

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: June 25, 2006, 08:01:28 ; Search time 1540 Seconds

(without alignments)
9590.739 Million cell updates/sec

Title: US-10-521-811-1

Perfect score: 1202

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues 37784340

Total number of hits satisfying chosen parameters:
Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA Main:*

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16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1202	100.0	1228	8 US-10-437-963-20266	Sequence 20266, A
2	420	34.9	454	10 US-10-487-901-6995	Sequence 6995, Ap
3	375.2	31.2	1276	8 US-10-425-114-3220	Sequence 3220, Ap
4	375.2	31.2	1352	8 US-10-374-780A-5568	Sequence 568, App
5	375.2	31.2	1352	8 US-10-412-6998-1061	Sequence 1061, Ap
6	372	30.9	1352	9 US-10-425-115-158957	Sequence 158957, A
7	366	30.4	1280	8 US-10-425-114-14357	Sequence 14357, A
8	366	30.4	1344	8 US-10-374-780A-5564	Sequence 564, App
9	366	30.4	1344	8 US-10-412-6998-1057	Sequence 1057, Ap
10	352.6	29.3	1126	8 US-10-425-114-24903	Sequence 24903, A
11	352.6	29.3	1492	8 US-10-374-780A-557	Sequence 567, App
12	352.6	29.3	1492	8 US-10-412-6998-1060	Sequence 1060, Ap
13	345.6	28.8	815	9 US-10-425-115-39025	Sequence 39025, A
14	345.6	28.8	1400	9 US-10-425-115-38157	Sequence 38157, A
15	331.2	27.6	1084	9 US-10-374-780A-5566	Sequence 566, App
16	331.2	27.6	1084	8 US-10-412-6998-1059	Sequence 1059, Ap
17	326.6	27.2	1074	3 US-09-443-704-3	Sequence 3, Appl

18	326.6	27.2	1074	6 US-10-008-118A-3	Sequence 3, Appl
19	324.6	27.0	777	8 US-10-437-963-90448	Sequence 90448, A
20	318.8	26.5	794	8 US-10-767-701-11055	Sequence 11055, A
21	315.6	26.3	1083	16 US-11-096-568A-25631	Sequence 25631, A
22	314.2	26.1	662	8 US-10-374-780A-555	Sequence 565, App
23	314.2	26.1	662	8 US-10-412-6998-1058	Sequence 1058, Ap
24	312.6	26.0	1086	8 US-10-425-114-1170	Sequence 1170, Ap
25	312.6	26.0	1088	9 US-10-425-115-151274	Sequence 151274, A
26	307.8	25.6	335	10 US-10-487-901-3480	Sequence 3480, Ap
27	302.8	25.2	643	8 US-10-374-780A-563	Sequence 563, App
28	302.8	25.2	643	8 US-10-412-6998-1056	Sequence 1056, App
29	296.8	24.7	866	9 US-10-425-115-27081	Sequence 27081, A
30	281.2	23.4	842	9 US-10-425-115-53108	Sequence 53108, A
31	278.8	23.2	577	3 US-09-443-704-37	Sequence 37, Appl
32	278.8	23.2	577	6 US-10-008-118A-37	Sequence 37, Appl
33	274.6	22.8	1467	16 US-11-096-568A-20587	Sequence 20587, A
34	271.8	22.6	777	8 US-10-374-780A-1542	Sequence 1542, Ap
35	271.8	22.6	777	8 US-10-412-6998-1636	Sequence 1636, Ap
36	269.2	22.4	1216	8 US-10-437-963-7945	Sequence 7945, Ap
37	249.8	20.8	804	8 US-10-437-963-68443	Sequence 68443, A
38	247.4	20.6	1116	8 US-10-437-963-55050	Sequence 55050, A
39	246	20.5	1212	8 US-10-437-963-39218	Sequence 39218, A
40	245.8	20.4	1023	8 US-10-437-963-84195	Sequence 84195, A
41	244.6	20.3	1285	8 US-10-425-114-31390	Sequence 31390, A
42	244.6	20.3	1285	9 US-10-425-115-75772	Sequence 75772, A
43	244.6	20.3	1302	8 US-10-374-780A-1543	Sequence 1543, Ap
44	244.6	20.3	1302	8 US-10-412-6998-1637	Sequence 1637, Ap
45	243	20.2	1427	6 US-10-021-811-25	Sequence 25, Appl

ALIGNMENTS

RESULT 1
US-10-437-963-20266
Sequence 20266, Application US/10437963
Publication No. US20040123343A1.
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 20266
LENGTH: 1228
TYPE: DNA
ORGANISM: Oryza sativa
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4530_25649C.1
US-10-437-963-20266
Query Match 100.0%; Score 1202; DB 8; Length 1228;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CAGCCGCTCCCTCCAGAACACACAGCAAGAGACGAGCAGTTCAGATCAGAC 60
DB 24 CAGCCGCTCCCTCCAGAACACACAGCAAGAGAGACAGCAGTTCAGATCAGAC 83
QY 61 AGGGAAGAGCAAGCAATGGGAGGCTCCGCTGCGAGAAATGGGGCTCAAGAAG 120
DB 84 AGGGAAGAGCAAGCAATGGGAGGCTCCGCTGCGAGAAATGGGGCTCAAGAAG 143
QY 121 GGTGATGAGCGCGGAGAGAGCAAGTCTGTCGTCGCCACATCCAGCGCCAGCGCAC 180

Db 144 GGTCCATGACGCGGAGAGAGCAAGTCTCTGTGCCCACTCCAGGCCACCGCCAC 203
Qy 181 GGGAACTGGCGCGCCCTGCCCAAGACCGGGCTCTGCTGGCGCAAGAGCTGCCG 240
Db 204 GGCACATGGCGCGCCCTGCCCAAGACCGGGCTCTGCTGGCGCAAGAGCTGCCG 263
Qy 241 CTCGGGTGATCAACTACCTGGCGCGGACATCAAGCGGGGCACTTCTCCAAAGAGAG 300
Db 264 CTCGGGTGATCAACTACCTGGCGCGGACATCAAGCGGGGCACTTCTCCAAAGAGAG 323
Qy 301 GAGGACACCATCATCCATCTCCAGAGCTGTTGGCAAGGTGTCTCCAAATGGCGCG 360
Db 324 GAGGACACCATCATCTCCAGAGCTGTTGGCAAGGTGTCTCCAAATGGCGCG 383
Qy 361 AGGTGCGCGGAG 420
Db 384 AGGTGCGCGGAG 443
Qy 421 GCGCTGATGCGCGGCTGAGGGCGGCTCATGTGCGGCGAGGGCGGCGAGAGAGAGAG 480
Db 444 GCGCTGATGCGCGGCTGAGGGCGGCTCATGTGCGGCGAGGGCGGCGAGAGAGAGAG 503
Qy 481 AAGCGGAG 540
Db 504 AAGCGGAG 563
Qy 541 GCGTCCGCTCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
Db 564 GCGTCCGCTCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 623
Qy 601 GCGGACGCGGAGATCAAGCTCGGCGGCTCGGCGGCTCGGCGGAGAGAGAGAGAG 660
Db 624 GCGGACGCGGAGATCAAGCTCGGCGGCTCGGCGGCTCGGCGGAGAGAGAGAGAG 683
Qy 661 ACCCTGGCTTCGAGAGAGTTCAGATCGAGAGAGTTCGATCGGAGAGAGAGAGAG 720
Db 684 ACCCTGGCTTCGAGAGAGTTCAGATCGAGAGAGTTCGATCGGAGAGAGAGAGAG 743
Qy 721 CCGCTGGAGAGAGTTCAGATCGAGAGAGTTCGATCGGAGAGAGAGAGAGAGAG 780
Db 744 CCGCTGGAGAGAGTTCAGATCGAGAGAGTTCGATCGGAGAGAGAGAGAGAGAG 803
Qy 781 GCGGACGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 840
Db 804 GCGGACGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 863
Qy 841 CCGGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 900
Db 864 CCGGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 923
Qy 901 TCTCTCTGCGCGCATCTTTCAGACCGGAGAGATGAGATGAGATGAGATGAGATGAG 960
Db 924 TCTCTCTGCGCGCATCTTTCAGACCGGAGAGATGAGATGAGATGAGATGAGATGAG 983
Qy 961 GCGGATCATCAAG 1020
Db 984 GCGGATCATCAAG 1043
Qy 1021 TAGCTTGAATGATTAATTTCTTTTTCATCTCTCTCTCTCTCTCTCTCTCTCTCT 1080
Db 1044 TAGCTTGAATGATTAATTTCTTTTTCATCTCTCTCTCTCTCTCTCTCTCTCTCT 1103
Qy 1081 ATCACTGATCAAACTGATGATCTTTCAGAGATGAGATGAGATGAGATGAGATGAG 1140
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Qy 1141 GCGCTGCGTCT 1200
Db 1164 GCGCTGCGTCT 1223
Qy 1201 AA 1202

Db 1224 AA 1225
RESULT 2
US-10-487-901-6995
; Sequence 6995, Application US/10487901
; Publication No. US20050091708A1
GENERAL INFORMATION:
; APPLICANT: Oreido, Jeremiah Vincent
; APPLICANT: McCreary, David
; APPLICANT: Pell, Randy
; APPLICANT: Miller, Barbara
; APPLICANT: Wedgarte, Thaddeus
; APPLICANT: Gachotte, Daniel
; APPLICANT: Blakeslee, Beth
; APPLICANT: Larrinua, Ignacio
; APPLICANT: Shukla, Vipula
; APPLICANT: Crosley, Rodney
; TITLE OF INVENTION: Nucleic Acid Compositions Conferring Altered Metabolic Characteri
; FILE REFERENCE: DOM-08552
; CURRENT FILING DATE: 2004-02-26
; NUMBER OF SEQ ID NOS: 7560
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6995
; LENGTH: 454
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-487-901-6995
Query Match 34.9%; Score 420; DB 10; Length 454;
Best Local Similarity 98.8%; Pred. No. 2.1e-111;
Matches 423; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 1 CAGCGGCTCCCTTCCAGAGACACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 60
Db 27 CAGCGGCTCCCTTCCAGAGACACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 86
Qy 61 AGGAG 120
Db 87 AGGAG 146
Qy 121 GGTCCATGAG 180
Db 147 GGTCCATGAG 206
Qy 181 GCGGACGAG 240
Db 207 GCGGACGAG 266
Qy 241 CTCGGGTGATCAACTACCTGCGCGGAGATCAAGCGGGCACTTCTCCAAAGAGAGAG 300
Db 267 CTCGGGTGATCAACTACCTGCGCGGAGATCAAGCGGGCACTTCTCCAAAGAGAGAG 326
Qy 301 GAGGACACCATCATCTCTCCAGAGCTGTTGGCAAGGTGTCTCCAAATGGCGCG 360
Db 327 GAGGACACCATCATCTCTCCAGAGCTGTTGGCAAGGTGTCTCCAAATGGCGCG 386
Qy 361 AGGTGCGCGGAG 420
Db 387 AGGTGCGCGGAG 446
Qy 421 GCGCTCGA 428
Db 447 GCGCTCGA 454
RESULT 3
US-10-425-114-3220
; Sequence 3220, Application US/10425114

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/ Publication No. US20040034888A1
/ GENERAL INFORMATION:
/ APPLICANT: Liu, Jingdong
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Screen, Steven E
/ APPLICANT: Tabaka, Jack E
/ APPLICANT: Cao, Yongwei
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
/ TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
/ FILE REFERENCE: 38-21(5313)B
/ CURRENT APPLICATION NUMBER: US/10/425,114
/ NUMBER OF SEQ ID NOS: 73128
/ SEQ ID NO 3220
/ LENGTH: 1276
/ TYPE: DNA
/ ORGANISM: Zea mays
/ FEATURE:
/ OTHER INFORMATION: Clone ID: 700243864_FLI
US-10-425-114-3220

Query Match          31.2%; Score 375.2; DB 8; Length 1276;
Best Local Similarity 64.6%; Pred. No. 3,7e-98;
Matches 711; Conservative 0; Mismatches 308; Indels 81; Gaps 7;

QY 76 ACAATGGGAGGGCTCGTCTGCGAGAAAGATGGGCTCAAGAAAGGCTCCATGACGCGG 135
DB 171 AGAATGGGAGAGCTCGTCTGCGAGAAAGATGGGCTCAAGAAAGGCGCATGACGCGG 230
QY 136 GAGGAGGAGAGGCTCTCGTCTGCGAGAAAGATGGGCTCAAGAAAGGCTCCATGACGCGG 195
DB 231 GAGGAGGAGAGATCTGCTGCGAGAAAGATGGGCTCAAGAAAGGCTCCATGACGCGG 290
QY 196 CTGCCCAAGCAAGCGCGGCTGCTGCGAGAAAGATGGGCTCGGCTCGGATCAAC 255
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QY 316 CATCTCCAGAGGCTGTTGGCAACAGATGTCGCAATTGCGCGCGGAGTTCGCGGAGG 375
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QY 376 ACGGCAACGAGATCAAGAAAGTGTGGCAACCCACCTCAAGAAAGCGCTCGATGCGGC- 434
DB 471 ACGGCAACGAGATCAAGAAAGTGTGGCAACCCACCTCAAGAAAGCGCTCGATGCGGC 530
QY 435 -----GCTCAGGCGGCTCATGTGCGGCGGAGCGGC 465
DB 531 ACCAAGCAGCTGAGAGCAGAGCAGCAGCGGCGCATGAGTGTGACCGCGCAGAGAG 590
QY 466 GCGCAAGAACAGAAAGCGCGAAGAGCGGAGAAACCGCGCGCGCGCGCGCGCGCG 525
DB 591 CCGAGAGGCGCGCAAGCGCGGCGTGCAGAGCAAGAGCGCGCGCGCGCGCGCGCG 650
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DB 651 GCGACACCGCGCGCGCGCTGCTGTAACGTCGCGCGCGCTCGCTGCTGAGTCCGATG 710
QY 586 GTGGCGGAGAGAGCAGCGCAAGCGCGGAGATCAAGTCCGCGCTCGCGCTGTCGCGCAAG 645
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QY 646 GAGGAGAGCTCTCTCACTCTGCGCTTCCGAGAGTTCAGATGAGAGACAGAGCTTCGATG 705
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QY 745 ATGAGACCCCGGAGACCGCTTCTGCGCGCGCCATCCG-----CGAGCAG 789
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QY 790 ATGACTACTGCTGCGAGTGTTCATGAGATCGCGCGAGCG---CAAGCTTGGCGAG 846
DB 948 TTGACTACTGCTGCGAGTGTTCATGAGATCGCGCGAGCGCGAGCAACTGCGCGAG 1007
QY 847 ATCTAGAG-----AAAGAGAGAAATTTTACCGTTCTTCCGTTAATTGAT--TTGTT 897
DB 1008 GTTTAGAGCGCGCAGCGCGCGCGAGAAATTTTACGTTCTTCCGTTAATTGATTCATGTT 1067
QY 898 TTTTCTCTCTGCGCGCGCATTTTGCACCGGAGGAGATAGCTAACAGAGAGTCCCA 957
DB 1068 CTTTCTCTCTCTGCGCGCGCTTTCGAAATTCGAGAGGAGACAGTCAATATACAGC 1127
QY 958 TGAGCGATCATCAAGCAGAGAAACGCAATCATCGATGCGATGAGATGACACC 1017
DB 1128 TAATTATAGAGGAGTGTGTGTTGAGAGACACGACGAGATTAGAGAGAAACAGCGCA 1187
QY 1018 CAGTACCTTGAATGTAATTTTCTTTTAACTCTTCTGTATGTATAGAAACAGAA 1077
DB 1188 CATGCCATTGACATCTATCTGTGCTTCTTGTGCTTCTGTATATAAAGATCATGATCGACAA 1247
QY 1078 GAGATCAGTATCGAAACT 1097
DB 1248 GATATCGTATCGAAACT 1267

RESULT 4
US-10-374-780A-568
/ Sequence 568, Application US/10374780A
/ Publication No. US20040019927A1
/ GENERAL INFORMATION:
/ APPLICANT: Sherman, Bradley K
/ APPLICANT: Riechmann, Jose Luis
/ APPLICANT: Jiang, Cai-Zhong
/ APPLICANT: Heard, Jacqueline E
/ APPLICANT: Haake, Volker
/ APPLICANT: Creelman, Robert A
/ APPLICANT: Ratcliffe, Oliver
/ APPLICANT: Adam, Luc J
/ APPLICANT: Reuber, T. Lynne
/ APPLICANT: Keddie, James
/ APPLICANT: Brown, Pierre E
/ APPLICANT: Pilgrim, Marsha L
/ APPLICANT: Dubell III, Arnold T
/ APPLICANT: Pineda, Omaria
/ APPLICANT: Yu, Guo-Liang
/ TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES IN PLANTS
/ FILE REFERENCE: MBI-0047 CIP
/ CURRENT APPLICATION NUMBER: US/10/374,780A
/ PRIOR FILING DATE: 2003-02-25
/ PRIOR APPLICATION NUMBER: 09/837,944
/ PRIOR FILING DATE: 2001-04-18
/ PRIOR APPLICATION NUMBER: 60/310,847
/ PRIOR FILING DATE: 2001-08-09
/ PRIOR APPLICATION NUMBER: 09/934,455
/ PRIOR FILING DATE: 2001-08-22
/ PRIOR APPLICATION NUMBER: 60/336,049
/ PRIOR FILING DATE: 2001-11-19
/ PRIOR APPLICATION NUMBER: 60/338,692
/ PRIOR FILING DATE: 2001-12-11
/ PRIOR APPLICATION NUMBER: 10/171,468
/ PRIOR FILING DATE: 2002-06-14
/ PRIOR APPLICATION NUMBER: 10/225,066
/ PRIOR FILING DATE: 2002-08-09
/ PRIOR APPLICATION NUMBER: 10/225,067
/ PRIOR FILING DATE: 2002-08-09
/ PRIOR APPLICATION NUMBER: 10/225,068
/ PRIOR FILING DATE: 2002-08-09
/ NUMBER OF SEQ ID NOS: 2906
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Query Match 31.2%; Score 375.2; DB 8; Length 1352;
Best Local Similarity 64.6%; Pred. No. 3.8e-98;
Matches 711; Conservative 0; Mismatches 308; Indels 81; Gaps 7;

76 ACAATGGGAGGAGCTCCGTCTCGAGAGATGGGGCTCAAGAAGGCTCATGAGCGCC 135
195 AGAATGGGAGAGCTCCGTCTCGAGAGATGGGGCTCAAGAAGGCGCATGAGCGCC 254
136 GAGGAGAGCAAGGTCTCTCGTCCCAATCCAGCGCCACGCGCAACCTGGCGCC 195
255 GAGGAGAGCAAGATCTCTGCTCGCGCAATCCAGAGCTTCGCGCACAGCAACTGGCGCG 314
196 CTGGCCCAAGCAAGCCCGGCTGCTGCTGCTGCGCAAGAGCTCCGCTCGGTGATCAAC 255
315 CTGGCCCAAGCAAGCCCGGCTGCTGCTGCGCAAGAGCTCCGCTCGGTGATCAAC 314
256 TACCTGCGCGCGGACATCAAGCGGGCAACTTCTCCAGAGAGAGAGACATCATC 315
375 TACCTGCGCGCGGACATCAAGCGGGCAACTTCCAGAGAGAGAGAGAGAGAGAGAG 434
316 CATCTCCAGAGAGCTCTGGCAACAGGTGCTCGCAATTCGCGCAGGTTGCCGGAGG 375
435 ACCCTCCAGAGAGAGCTCGGCAACAGGTGCTCGCGCATCGCGCAGGCTGCCGGAGG 494
376 ACCGAGCAAGAGATCAAGAACTGTGGCAACCCACTTCAAGAGAGCGCTCATGCGCC 434
495 ACCGAGCAAGAGATCAAGAACTGTGGCAACCCACTTCAAGAGAGCGCTCGAGGCCACC 554
435 -----GGCTCAGGCGCGGTATGTCGCGCGGAGCGCG 465
555 ACCAGCACTGAG 614
466 GGCAG 525
615 CCAG 674
526 CCGGCTCGCGCGAG 585
675 GGCAG 734
586 GTGGCGAG 645
735 AGGAG 791
646 GAG 705
792 ACCTTCACTCGTCTCGAG 851
706 GAG 744
852 GAG 911
745 ATGAG 789
912 GCGCGCTTGGGAG 971
790 ATGAG 846
972 TTGAG 1031
847 ATCTAGAG-----AAGAGAGAGAGATTTTACCGTTTCTCGTTAATGAT---TTGTT 897
1032 GTTTTGAAGGCGGAG 1091
898 TTTTCTCTCTGCGCGCAATCTTGCACCGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 957
1092 CTTTCTCTCTCTGCGCGCAATCTTGCACCGAGAGAGAGAGAGAGAGAGAGAGAGAG 1151
958 TGAG 1017
1152 TAATTAAATGAG 1211

1018 CAGTACCTGATGATTAATTTCTTTTACCCTCTCTATGATAGAGAGAA 1077
1212 CAGCCATGATGATTAATTTCTTTTACCCTCTCTATGATAGAGAGAA 1271
1078 GAGATCAGTATGAGAAACCT 1097
1272 GATATCGTATGAGAAACCT 1291

RESULT 6
US-10-425-115-158957
; Sequence 158957, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21 (39222) B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ. ID NOS: 369326
; SEQ. ID NO 158957
; LENGTH: 1352
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_76543C.1
US-10-425-115-158957

Query Match 30.9%; Score 372; DB 9; Length 1352;
Best Local Similarity 65.0%; Pred. No. 3.2e-97;
Matches 714; Conservative 0; Mismatches 305; Indels 79; Gaps 8;

76 ACAATGGGAGGAGCTCCGTCTCGAGAGATGGGGCTCAAGAAGGCTCATGAGCGCC 135
197 AGAATGGGAGAGCTCCGTCTCGAGAGATGGGGCTCAAGAAGGCGCATGAGCGCC 256
136 GAGGAGAGCAAGGTCTCTCGTCCCAATCCAGCGCCACGCGCAACCTGGCGCGCC 195
257 GAGGAGAGCAAGATCTCTGCTCGCGCAATCCAGAGAGCTTCGCGCAACCTGGCGCGCC 316
196 CTGGCCCAAGCAAGCCCGGCTGCTGCTGCTGCGCAAGAGCTTCGCTCGGTGATCAAC 255
317 CTGGCCCAAGCAAGCCCGGCTGCTGCTGCGCAAGAGCTTCGCTCGGTGATCAAC 316
256 TACCTGCGCGCGGACATCAAGCGGGCAACTTCTCCAGAGAGAGAGAGAGAGAGAGAG 315
377 TACCTGCGCGCGGACATCAAGCGGGCAACTTCCAGAGAGAGAGAGAGAGAGAGAGAG 436
316 CATCTCCAGAGAGCTCTGGCAACAGGTGCTCGCAATTCGCGCAGGTTGCCGGAGAG 375
437 ACCCTCCAGAGAGAGCTCGGCAACAGGTGCTCGCATCGCGCCAGGCTGCCGGAGAG 496
376 AGGAG 431
497 ACCGAGCAAGAGATCAAGAACTGTGGCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 556
432 -----GCCGCTCAGGCGGCTGATGTCGCGCGAGAGAGAGAGAGAGAGAGAGAG 474
557 ACCAGCACTGAG 616
475 CACAG 527
617 CCGAG 676
528 GCGGCTCGCGCGAG 587
677 CACAG 736
588 GCGGAG 647


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QY 136 GAGGAGAGCAAGGCTCTCGTCCGCCACATCAGCGCCACGCGCAACGTGGCGGCC 195
DB 134 GAGGAGAGCAAGGCTCTCGTCCGCCACATCAGCGCTTGGGCCAAGCAATGGCGGCG 193
QY 196 CTGCCCAAGCAAGCGGGCTGCTGCTGGGGCAAGAGCTGCGGCTCCGGTGTGATCAAC 255
DB 194 CTGCCCAAGCAAGCGGGCTGCTGCTGGGGCAAGAGCTGCGGCTCCGGTGTGATCAAC 253
QY 256 TACCTCGCGCGGACATCAAGCGGGGCACTTCTCCAAAGAGAGGAGGACACATCATC 315
DB 254 TACCTCGCGCGGACATCAAGCGGGGCACTTCAAGAGAGAGAGAGAGGAGGACATCATC 313
QY 316 CATCTCCAGAGAGTGTGGCAACAGGTGTGTCGCAATTCGCGCAGGTTGCCGAGAG 375
DB 314 AGCCTCCAGAGAGTGTGGCAACAGGTGTGTCGCAATTCGCGCAGGTTGCCGAGAG 373
QY 376 ACGGACAAAGAGATCAAGAAAGTGTGGCACACCACTTCAAGAAAGGCTTCGATGC--- 431
DB 374 ACGGACAAAGAGATCAAGAAAGTGTGGCACACCACTTCAAGAAAGGCTTCGATGCCACC 433
QY 432 -----GCCGCGCTCAGGGCGGTGATGTGCGCGGCGAGCGCGCGGCAAGAACAC 477
DB 434 AAGCAGAGAGCAGAGCAGCAGCAGGAGCAGCGCGGCGGTGCGCGCGGCAAGAACAC 493
QY 478 AAGAAAGCGAAGAGCGCGAAG-----AGCCA 504
DB 494 AAGCGCGCAGCGCGCGGCGAAGCGCGGCGCGGCGGAGCCAGAAAGGCGAGCGCAACGCC 553
QY 505 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 555
DB 554 GACGCGGTGCTGCTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 613
QY 556 TCGGTGACGGAAGTCTCGATGAGGCTGTGCGGTGCGGAGAGAGAGAGAGAGCGGGAGTC 615
DB 614 TCGGCGCGCGCTCGTGTGCGGTGAGCAGAGTGTGCTCATACGAGAGAGAGAGAGAGAGCG 673
QY 616 AGCTCGCGCGCTCGCGCTGCTGTCGCGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 669
DB 674 AAGCAGGAGAGAGTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 733
QY 670 TCGGAGAGAGTTCAGATCGACGACAGCTTCTGTGTCGAGAGAGCGTGTGATGCGCTGGA- 728
DB 734 GCGGAGAGAGTTCAGATCGACGACAGCTTCTGTGTCGAGAGAGCGTGTGATGCGCTGGA- 793
QY 729 -----CGGGTACGAGCGTGTCCATGAGAGCGCGCGGAGAG----- 760
DB 794 AGCCTGACGAGCGTGTCTCCCATGAGAGCGCTTCGAGAGAGAGCGCGTTCGCGAGCGTGCAC 853
QY 761 -----CGTTGCTGCGCGCGCGCATCCGCGGACGACATGAGACTAGTGGCTCGA 807
DB 854 GTGGCTGCGCGCGCTCTCTCTGTCGTCGCGCGCGAGCGGAGCGGAGCTGAGCTAGTGGCTCAGA 913
QY 808 GTGTTCAAGAGTCTCGGCGAGAGCGCA---AGACTTCGCGAGATCTAGAGAAAGAGAGAG 864
DB 914 GTGTTCAAGAGTCTCGGCGAGAGCGGAGCGGAGAGCTGCGGAGATTTAGACCGGTCGCGG 973
QY 865 AATTTTACCGTTTCTTCCGTTAAT-----TGATTTGTTTCTCTCTGCGCGCATCT 919
DB 974 AATAATTTTGGCTCTTAATTTGATTCATGCTTTTGTCTCTCTCTCTCTCTCTCTCTCTCT 1033
QY 920 TGCACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 979
DB 1034 TGCATCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1093
QY 980 GAA 982
DB 1094 GAA 1096

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RESULT 11
 US-10-374-780A-567
 ; Sequence 567, Application US/10374780A
 ; Publication No. US20040019927A1

```

; GENERAL INFORMATION:
; APPLICANT: Sherman, Bradley K
; APPLICANT: Riechmann, Jose Luis
; APPLICANT: Jiang, Cai-Zhong
; APPLICANT: Heard, Jacqueline E
; APPLICANT: Haake, Volker
; APPLICANT: Creelman, Robert A
; APPLICANT: Ratcliffe, Oliver
; APPLICANT: Adam, Luc J
; APPLICANT: Reuber, T. Lyne
; APPLICANT: Keddie, James
; APPLICANT: Brown, Pierre E
; APPLICANT: Pilgrim, Marsha L
; APPLICANT: Dubell III, Arnold T
; APPLICANT: Pineda, Omaira
; APPLICANT: Yu, Guo-Liang
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES IN PLANTS
; FILE REFERENCE: MBI-0047 CIP
; CURRENT APPLICATION NUMBER: US/10/374,780A
; PRIOR FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: 09/837,944
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 60/310,847
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 09/934,455
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/336,049
; PRIOR FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/338,692
; PRIOR FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: 10/171,468
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 10/225,066
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/225,067
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/225,068
; PRIOR FILING DATE: 2002-08-09
; NUMBER OF SEQ ID NOS: 2906
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 567
; LENGTH: 1492
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Predicted polypeptide sequence is orthologous to G241
US-10-374-780A-567

Query Match 29.3%; Score 352.6; DB 8; Length 1492;
Best Local Similarity 66.8%; Pred. No. 1.5e-91;
Matches 683; Conservative 0; Mismatches 224; Indels 116; Gaps 8;

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QY      739 GT-----GTCATGAGCCCGCGACCGCGTTCTCGGCGG 774
Db      802 TTCAGTCCGGGTGCGAGCGCGAGCGGCGAGCTTCCGCGCGTGGCGGCGCGCCGTCG 861
QY      775 CCATCGCGCGACGACATGACTGAGTTCGAGTTCATGAGTCCGCGAAGCGCA 834
Db      862 TCGACCAACGACGACATGACTTCTGCTCAAGCTGTTCAATGCGAGCGACGACATGCA 921
QY      835 GACTTGGCGCGAGAT 848
Db      922 AATTGCCCGAGAT 935
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Search completed: June 25, 2006, 09:58:37
Job time : 1548 secs

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No.	Score	Match	Length	DB	ID	Description
1	201.4	16.8	766	3	US-09-640-211A-2027	Sequence 2027, Ap
2	199.8	16.6	648	3	US-09-640-211A-2036	Sequence 2036, Ap
3	195.8	16.3	1344	2	US-08-722-62EB-1	Sequence 2036, Ap
4	193.6	16.1	1046	3	US-09-533-029-6A	Sequence 1, Appli
5	193.4	16.1	4434	3	US-09-640-211A-1965	Sequence 61, Appl
6	192.6	16.0	563	3	US-09-640-211A-252	Sequence 1965, Ap
7	190.8	15.9	360	3	US-09-640-211A-1266	Sequence 252, Appl
8	190.8	15.9	513	3	US-09-640-211A-519	Sequence 1266, Ap
9	188	15.6	631	3	US-09-640-211A-1718	Sequence 519, Appl
10	188	15.6	1150	3	US-09-640-211A-2088	Sequence 1718, Ap
11	181.6	15.1	473	3	US-09-640-211A-2087	Sequence 2088, Ap
12	181.6	15.1	1576	3	US-09-640-211A-2105	Sequence 2087, Ap
13	181.2	15.1	636	3	US-09-640-211A-1797	Sequence 2105, Ap
14	180	15.0	509	3	US-09-640-211A-2071	Sequence 2075, Ap
15	179	14.9	373	3	US-09-640-211A-1982	Sequence 1797, Ap
16	179	14.9	373	3	US-09-640-211A-2071	Sequence 1982, Ap
17	178.4	14.8	311	3	US-09-640-211A-181	Sequence 2071, Ap
18	178.4	14.8	311	3	US-09-640-211A-189	Sequence 181, Appl
19	177.4	14.8	385	3	US-09-640-211A-2057	Sequence 281, Appl
20	173.4	14.4	544	3	US-09-640-211A-1987	Sequence 1499, Ap
21	170	14.1	476	3	US-09-640-211A-1987	Sequence 2057, Ap
22	165.6	13.8	351	3	US-09-640-211A-1684	Sequence 2020, Ap
23	165.6	13.5	2352	3	US-08-597-251-3	Sequence 1987, Ap
						Sequence 1684, Ap
						Sequence 3, Appli

QY 347 CCGCAATGCGCCGAGTGGCCGGGAGGACGAGCAAGATCAAGAAAGTGTGGACA 406
DB 540 CGCTGATACGGGACCGTTGGCCGGGAGAGACAGACAAAGATTAAAGACTACTGGACA 599
QY 407 CCCACCTCAAGAACCGCTCGATCGCC 433
DB 600 CCACATCAAGAGAAAGCTTACGGCAC 626

RESULT 2
US-09-640-211A-2036

; Sequence 2036, Application US/09640211A
; Patent No. 6833446
; GENERAL INFORMATION:
; APPLICANT: Wood, Marion
; APPLICANT: Shenk, Michael A.
; APPLICANT: McGrath, Annette
; APPLICANT: Glenn, Matthew
; TITLE OF INVENTION: Compositions and Methods for the
; TITLE OF INVENTION: Modification of Gene Transcription
; FILE REFERENCE: 11000.1021CIU
; CURRENT APPLICATION NUMBER: US/09/640,211A
; NUMBER OF SEQ ID NOS: 2368
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2036
; LENGTH: 648
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-09-640-211A-2036

Query Match 16.6%; Score 199.8; DB 3; Length 648;
Best Local Similarity 73.5%; Pred. No. 6.5e-13;
Matches 255; Conservative 0; Mismatches 92; Indels 0; Gaps 0;

QY 79 ATGGGAGGCGCTCCGTCTGCGAGAGATGGGCTCAAGAGGCTCATGACGCCGAG 138
DB 72 ATGGGAGGCAACCGTGTGTGCAAAATCCGGGTGAAGAAAGACCGTGGACGGCGAG 131
QY 139 GAGGACAAAGTCTCTCGGCCCATTCACAGCCGACGCGGCAACTGGCGCCCTG 198
DB 132 GAGGACAAAGTCTCTCAATTCATCTCACCAAGGCGCAGCTGCTGGCGGTGCTC 191
QY 199 CCCAAGCAAGCGCGGTGTGGTGGCGAAGAGCTGCGGCTCGGTGATCAATCAG 258
DB 192 CTTAGCTTCCGAGCTCCGCGCTCGCGGAGAGCTGCGCTCGGTGACCACTAC 251
QY 259 CTGCGGCCGAGATCAAGCGGGGCACTTCTCCAGAGAGAGAGACACATCATCAT 318
DB 252 CTCGCGCCGAGCTTCAAGCGGCGCTCTCAAGTGAAGAGAGAGAGCTCGTCAATCAG 311
QY 319 CTCACAGAGCTGTGGCAACAGTGTGCGCAATTCGCCGAGTTGCCGAGGAGAG 378
DB 312 CTCACAGCTCCGCTCGGCAACAGTGTGCAAGATGCGGCAAGTGTGCCGAGAAC 371
QY 379 GACCAAGATCAAGAAAGTGTGACACACCACTCAAGAGGCGCT 425
DB 372 GACCAAGAAATTAAGAACATTGGAACACCCACATCAAGAAAGCT 418

RESULT 3
US-08-722-626B-1

; Sequence 1, Application US/08722626B
; Patent No. 5939601
; GENERAL INFORMATION:
; APPLICANT: Yang, Yimong
; APPLICANT: Klesiss, Daniel, F.
; TITLE OF INVENTION: NOVEL GENES ASSOCIATED WITH ENHANCED
; TITLE OF INVENTION: DISEASE RESISTANCE IN PLANTS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dann, Dorfman, Herrell and Skillman
; STREET: 1601 Market Street Suite 720

; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103-2307
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/722,626B
; FILING DATE: 27-SEP-1996
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pat Hagan
; REGISTRATION NUMBER: 27,643
; REFERENCE/DOCKET NUMBER: 97-0010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215 563-4100
; TELEFAX: 215 563-4044
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1344 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 148...981
; OTHER INFORMATION:

US-08-722-626B-1

Query Match 16.3%; Score 195.8; DB 2; Length 1344;
Best Local Similarity 71.6%; Pred. No. 5.3e-32;
Matches 257; Conservative 0; Mismatches 102; Indels 0; Gaps 0;

QY 72 AAGCAATATGGGAGGCTCCGTCTGCGAGAAAGTGGGCTCAAGAGGCTCATGAC 131
DB 141 AAAGAAATGTGAGAGCTCTTGTGTGAGAAATGGGCTGAAGAAAGGCGCATGAT 200
QY 132 GCCGAGAGAGCAAGTCTGTGCGCCCAATCCAGCGCCAGCGCAACTGGCG 191
DB 201 TCTCAAGAAATCAAGATTTCTATCTTTTCAATTAAGCTAATGCGCAACTGGCG 260
QY 192 CGCCTTCCCAAGACCGGCGCTGCTGCTGGCGCAAGAGCTCCGCTCGGTGAT 251
DB 261 AGCCCTTCCCAAGACCGCTGACTATTAAGATGCGGAAAGTTGACAGCTCGGTGAC 320
QY 252 CAATCACTGCGCGCGGACATCAAGCGGGGCACTTCTCCAGAGAGAGAGACCAT 311
DB 321 GAATTAATTTGCGACCAATATTAAGAGGGGAAATTTCAACCAAGAGAGAGAAACAT 380
QY 312 CATCATCTCCACGAGCTGTGGCAACAGGTGTCCGCAATTTGCCGAGGTTGCCCG 371
DB 381 TATCAAGTAACTGAATGCTTTGGCAATAGATGCTTCCATAGACGCAAAATTAACAG 440
QY 372 GAGGACGAGCAACGAGATCAAGAACGTGTGCAACCACTCAAGAACCGCTGATG 430
DB 441 AGGACAGCAATGAATTAAGAAATGTTGGCACACCACTTGAAGAGAAAGCTCAAG 499

RESULT 4

US-09-533-029-61
; Sequence 61, Application US/09533029

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; Patent No. 6664446
; GENERAL INFORMATION:
; APPLICANT: Heard, Jacqueline
; APPLICANT: Broun, Pierre
; APPLICANT: Riechmann, Jose-Luis
; APPLICANT: Keddie, James
; APPLICANT: Pineda, Omartra
; APPLICANT: Adam, Luc
; APPLICANT: Samaha, Raymond
; APPLICANT: Zhang, James
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ratcliffe, Oliver
; APPLICANT: Pilgrim, Marsha
; APPLICANT: Jiang, Cai-zhong
; APPLICANT: Reuber, Lynne
; TITLE OF INVENTION: DISEASE-INDUCED POLYNUCLEOTIDES
; FILE REFERENCE: MBI-010
; CURRENT APPLICATION NUMBER: US/09/533,029
; CURRENT FILING DATE: 2000-03-22
; EARLIER APPLICATION NUMBER: 60/125,814
; EARLIER FILING DATE: 1999-03-23
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: Patent Ver. 2.1
; SEQ ID NO 61
; LENGTH: 1046
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; OTHER INFORMATION: G233
US-09-533-029-61
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Query Match      16.1%; Score 193.6; DB 3; Length 1046;
Best Local Similarity 71.9%; Pred. No. 1.5e-31;
Matches 253; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

QY 79 ATGGGAGGGCTCCGCTGCTGCGAGAGATGGGGCTCAAGAAAGGCTCATGAGCGCCGAG 138
DB 46 ATGGGAGAGCTCCATGCTGCTGAGAGATGGGGTTGAAGAGAGACATGACACCTGAA 105
QY 139 GAGGACAGAGTCTCTGCTGCCCATCCAGCGCCACGCGACCGCAACTGGCGCGCCCTG 198
DB 106 GAAGATCAATCTTGGTCTCTTTATCTCAACATGACATAGTAAGTGGCGAGCCCTC 165
QY 199 CCCAAGCAAGCCGGGCTGCTGCTGCGGCAAGAGCTGCCGGTCCGGTGGATCAATC 258
DB 166 CCTAAGCAAGCTGGGCTTTTGAATGTGAAAAAGCTGTAAGACTTGGGATGAAC 225
QY 259 CTGGGCGGAGCATCAAGCGGGGCACTTCTCCAGAGAGAGAGACACATCATCAT 318
DB 226 TTAAGCTGATATTAAAGCTGGCAATTTCCACCAAGAGAGAGATGCTATCATCAGC 285
QY 319 CTCACGAGCTGTTGGCAACAGGTGTCGCAATTGCCGACGTTGCCCGGAGAGAGC 378
DB 286 TTACACCAATACTTGGCAATAGATGTCAGGATTGCAGCAAACTGCCTGGAGAAC 345
QY 379 GACCAAGATCAAGAGCTGTGGCAACCCACCTCAAGAGCGCTCCATG 430
DB 346 GATTAAGAGATCAAGAACGTATGGCACCTCACTTAAGAGAGACTCGAAG 397
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RESULT 5
US-09-640-211A-1965
; Sequence 1965, Application US/09640211A
; Patent No. 6833446
; GENERAL INFORMATION:
; APPLICANT: Wood, Marion
; APPLICANT: Shenk, Michael A.
; APPLICANT: McGrath, Annette
; APPLICANT: Glenn, Matthew
; TITLE OF INVENTION: Compositions and Methods for the
; FILE REFERENCE: 11000.1021CIU
; CURRENT APPLICATION NUMBER: US/09/640,211A
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; CURRENT FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 2368
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1965
; LENGTH: 424
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-09-640-211A-1965
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Query Match      16.1%; Score 193.4; DB 3; Length 424;
Best Local Similarity 69.4%; Pred. No. 1.3e-31;
Matches 263; Conservative 0; Mismatches 116; Indels 0; Gaps 0;

QY 58 ACAGGAGAGAGCAAGCAACATGGGAGAGGCTCCGTGCTGGAGAAATGGGGCTCAAG 117
DB 25 ACCGGAGCGAGAGGAGAGCGATGGGACGAGCCCTGCTGGACAAAGCTTGGGGTGAAG 84
QY 118 AAGGTCATGAGACGCGGAGAGAGCAAGTCTCTGCTGCCACATCCAGCGCCACGCG 177
DB 85 AAAGGCGCTGAGACGCGGAGAGAGACCGGAAGCTGTCAATTCATCAACCCAGCGC 144
QY 178 CACGGCACTGGCGCGCTTCCCAAGCAAGCGGGCTGTGGCTTGGCGCAAGAGCTGC 237
DB 145 CATGCTGTGGCGCGCGCTCCCAAGCTGCTGGGCTCCGCGCTGTGGCAAGAGCTGC 204
QY 238 CGGCTCCGCTGATCAACTAAGCTGCGCGGACATCAAGCGGGCAACTTCTCCAGAG 297
DB 205 CGCTTCGCTGAGCAACTAAGCTGCGCGGATCTCAAGCGGCTCTCAATGAAGCC 264
QY 298 GAGGAGACACCATCATCTCCAGAGCTGTGGCAAGAGTGTGCCCAATTGGC 357
DB 265 GAGGAAGCTGTGATTCATCTCCATGCACTTCGGCAATAGGTGCTCAAAATAGCA 324
QY 358 GCCAGTTCGCGGAGAGAGCAAGATCAAGAGTGTGGCAAGCTGTGGCAAGCTCAAG 417
DB 325 GCTAGACTACCGGAAGAGCAAGCAAGATCAAAACCACTGGAAACCATATCAAG 384
QY 418 AAGCGCTGATGCGCGCG 436
DB 385 AAGAGCTCATTAAGATGG 403
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RESULT 6
US-09-640-211A-252
; Sequence 252, Application US/09640211A
; Patent No. 6833446
; GENERAL INFORMATION:
; APPLICANT: Wood, Marion
; APPLICANT: Shenk, Michael A.
; APPLICANT: McGrath, Annette
; APPLICANT: Glenn, Matthew
; TITLE OF INVENTION: Compositions and Methods for the
; FILE REFERENCE: 11000.1021CIU
; CURRENT APPLICATION NUMBER: US/09/640,211A
; NUMBER OF SEQ ID NOS: 2368
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 252
; LENGTH: 563
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-09-640-211A-252

Query Match      16.0%; Score 192.6; DB 3; Length 563;
Best Local Similarity 72.5%; Pred. No. 2.1e-31;
Matches 263; Conservative 0; Mismatches 99; Indels 1; Gaps 1;

QY 55 CAGAGCAGGAGAGAGAGCAACATGGGAGAGGCTCCGTGCTGGCAAGAGATGGGGCTC 114
DB 193 CAGAGGCTGCGCGCGAGAGAGATGGGAGATCCCTTGTGTGGCAAGAGCGCACACC 252
QY 115 AAGAGGTCATGAGCGCGGAGAGAGCAAGTCTCTGCTGCCACATCCAGCGCAC 174
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Db      253 AACAAAGGGCGGCTGATGACCAAGAGAGACCAAGCGCTTCAATGACATACATCCGCCCTCCAC 312
Qy      175 GGGCCACGGCAATGCGGCGGCGCTGCGCAAGCAACCGGGGCTGCTGGTTGGCGCAAGAC 234
Db      313 GGGCAAGGTTGGCTGGGCGCTCCCTCCCAATCTGCGGGCTTCTCGAGTGGCGCAAGAC 372
Qy      235 TGGCGGCTCGGGGATGATCACTACCTGCGGCGGACATCAAGGGGGCAACTTCTCCAG 294
Db      373 TGCAGGCTCAGGTGATTAATCTACCTCCGCGCCGACCTC-AGCGCGCAACTTCAACCGAG 431
Qy      295 GAGAGAGAGACACCATCACTCACTTCCAGAGCTCTTGGCAACAGTGTCCGCAAT 354
Db      432 GAAAGAGAGAGAGTCACTCAAGCTCCACAGCTTCTGGCAACAGTGTCTGATC 491
Qy      355 GCGCGCAGGTTGCGCGGAGAGACGCAACAGATCAAGACTGTGGCAACCCACCTC 414
Db      492 GCGGGAGATTGCCCGGAAGAACGACAGATCAAGACTGGAACACCCACATC 551
Qy      415 AAG 417
Db      552 AAG 554
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RESULT 7

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US-09-640-211A-1266
; Sequence 1266, Application US/09640211A
; Patent No. 6833446
; GENERAL INFORMATION:
; APPLICANT: Wood, Marion
; APPLICANT: Shenk, Michael A.
; APPLICANT: McGrath, Annette
; APPLICANT: Glenn, Matthew
; TITLE OF INVENTION: Compositions and Methods for the
; FILE OF INVENTION: Modification of Gene Transcription
; FILE REFERENCE: 11000.1021CIU
; CURRENT APPLICATION NUMBER: US/09/640,211A
; NUMBER OF SEQ ID NOS: 2368
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1266
; LENGTH: 360
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-09-640-211A-1266
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Query Match      15.9%; Score 190.8; DB 3; Length 360;
Best Local Similarity 73.4%; Pred. No. 4.5e-31;
Matches 257; Conservative 0; Mismatches 92; Indels 1; Gaps 1;
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Qy      68 GAGCAAGCAATGGGAGGCGTCCGTGCGAGAAAGATGGGGCTCAAGAGGCTCAT 127
Db      3 GCGCAGCAACATGGAGCATGCCCTTGTGCTGCGAAGAGCGCACACCAAGGCGCT 62
Qy      128 GAGCGCGGAGAGAGCAAGAGTCTGTCGCCCACTCAAGCGCCACGCGCACT 187
Db      63 GAGCAAGAGAGAGAGCAAGCGGCTCATGACTACGCGCTCCACGCGAAGTTGCT 122
Qy      188 GGGCGGCGGCTGCGCAAGCAAGCGGCTGCTGCTGGCGCAAGAGCTCCGGCTCCGT 247
Db      123 GGGCGCTCCCTCCCAATCTGCGGGCTTCTCAAGGCGCAAGAGCTCAAGGCT 182
Qy      248 GATCACTACTACCTGCGGCGGACATCAAGGGGGCACTTCTTCAAGAGAGAGAGCA 307
Db      183 GATTAATCACTCTCCGCGCGGCTCAAG-CCGCGCAACTTCAACGAGAGAGAGAGAC 241
Qy      308 CCATCACTCACTTCCAGAGCTGCTTGGCAACAGTGTGTCGCAATYGGCGCGAGTTGC 367
Db      242 TCATCACTCAAGCTCCACAGCTTCTGCGCAACAGTGTCTGATGCGGGGAGATTGC 301
Qy      368 CCGGAGAGAGAGCAACAGATCAAGAGAGTGTGGACACCCACCTCAAG 417
Db      302 CCGGAAGAACGACCAAGAGATCAAGACTGGAACACCCACATCAAG 351
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RESULT 8

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US-09-640-211A-519
; Sequence 519, Application US/09640211A
; Patent No. 6833446
; GENERAL INFORMATION:
; APPLICANT: Wood, Marion
; APPLICANT: Shenk, Michael A.
; APPLICANT: McGrath, Annette
; APPLICANT: Glenn, Matthew
; TITLE OF INVENTION: Compositions and Methods for the
; FILE OF INVENTION: Modification of Gene Transcription
; FILE REFERENCE: 11000.1021CIU
; CURRENT APPLICATION NUMBER: US/09/640,211A
; NUMBER OF SEQ ID NOS: 2368
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 519
; LENGTH: 513
; TYPE: DNA
; ORGANISM: Pinus radiata
US-09-640-211A-519
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Query Match      15.9%; Score 190.8; DB 3; Length 513;
Best Local Similarity 71.2%; Pred. No. 4.9e-31;
Matches 252; Conservative 0; Mismatches 102; Indels 0; Gaps 0;
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Qy      74 GCACAAATGGGAGGCGCTCCGTGCTGCGAGAGATGGGCTCAAGAGGCTCATGAGCC 133
Db      71 GCACCATGGGCGGAGCTCTTGTGCTGATTAATGGAGTAAAGAGCGCTGAGATC 130
Qy      134 CGAGAGAGAGAGAGTCTCCGTCGCGCCACATCCAGCGCACAGCGCAACTGGCGCG 193
Db      131 TAGACGAAGATTAATTAATCTGTCGATTAATTAACAAATGCGCACTGGCACTGGCGC 190
Qy      194 CCTGCCCAAGCAAGCGGCTGCTGCTGCTGGCGAGAGCTCCGCTCCGGTGGATCA 253
Db      191 CACTGCCCAAGCAAGCAAGGCTCTGCGATGTGGAAGAGTGTGCGCTCGGTTGAGCA 250
Qy      254 ACTACCTGGCGCGGAGCATCAAGCGGCGCACTTCTCAAGAGAGAGAGACACCATCA 313
Db      251 ACTACCTGAACCCACACATCAAAAGAGGAATTTAGTCCAGAAAGAGATCAAAATTA 310
Qy      314 TCCATCTCCAGAGCTGCTGGCAACAGATGTCGCAATTCGCCGAGGTTGCCCGGGA 373
Db      311 TTAAATTGATGATGCTCATAGGGAATAGATGCTCACTAATTTCTTCTGTTCCAGAGA 370
Qy      374 GAGCGAGACAAGATCAAGAAAGTGTGGCACACCCACCTCAAGAGCGCTCG 427
Db      371 GAACCGACAATGATCAAGAAAGTGTGGAACACCATTTAAAGAAAGTGTGCG 424
RESULT 9
US-09-640-211A-1718
; Sequence 1718, Application US/09640211A
; Patent No. 6833446
; GENERAL INFORMATION:
; APPLICANT: Wood, Marion
; APPLICANT: Shenk, Michael A.
; APPLICANT: McGrath, Annette
; APPLICANT: Glenn, Matthew
; TITLE OF INVENTION: Compositions and Methods for the
; FILE OF INVENTION: Modification of Gene Transcription
; FILE REFERENCE: 11000.1021CIU
; CURRENT APPLICATION NUMBER: US/09/640,211A
; NUMBER OF SEQ ID NOS: 2368
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1718
; LENGTH: 631
; TYPE: DNA
; ORGANISM: Pinus radiata
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US-09-640-211A-1718

Query Match 15.6%; Score 188; DB 3; Length 631;
Best Local Similarity 72.1%; Pred. No. 2e-30;
Matches 245; Conservative 0; Mismatches 95; Indels 0; Gaps 0;

QY 79 ATGGGAGGAGCTCCGCTGTCGAGAAAGATGGGGCTCAAGAGGGTCCATGAGACGGCGAG 138
DB 107 ATGGGAGAGATCTCTCGTCTGTGAAAAAGCTCATACAAACAAAGGGCGTGGACAAAGAA 166
QY 139 GAGGACAAAGTCTCTGTCGCCCATTCACGCGCCAGCGCCACGCAATGGCGCGCTTG 198
DB 167 GAGGACGATGCGCTTCATTCGCCCATTCGAACTCAGGGGAAAGTTGGCGGCTGCTT 226
QY 199 CCCAAGCAAGCCGGGCTGCTGCTTGGCGCAAGAGCTCCGGCTCCGGTGGATCAACTAC 258
DB 227 CCCAAGCCGCGAGGGCTGATGCGCTCGGGAAAGAGCTGACGGCTCCGATGATMAACTAC 286
QY 259 CTGCGGCGGAGCATCAAGGGGGGCACTTCTCCAAGGAGGAGGACACCATCATTCAT 318
DB 287 CTGCGTCTGATTTGAAGCGTGAAACCTTCTCAGAAAGAGACGAACTGTCATCAAA 346
QY 319 CTCACGAGCTGCTTGGCAACAGGTGATCGCAATTGCGGCCAGTTGCCCGGAGAGAG 378
DB 347 CTCACCTCCCTACTCGGCAACAGTGTCTCTATTGCAAGGCGAGATTGCCCGGGGAG 406
QY 379 GACAAAGATCAAGAACGCTGTGGCAACCCACCTCAAGA 418
DB 407 GACAAAGATMAAGAACTACTGGAATACTACATCAAGA 446

RESULT 10

US-09-640-211A-2088
; Sequence 2088, Application US/09640211A
; Patent No. 6833446
; GENERAL INFORMATION:
; APPLICANT: Wood, Marion
; APPLICANT: Shenk, Michael A.
; APPLICANT: McGrath, Annette
; TITLE OF INVENTION: Compositions and Methods for the
; FILE REFERENCE: 11000.1021CIU
; CURRENT APPLICATION NUMBER: US/09/640,211A
; CURRENT FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 2368
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2088
; LENGTH: 1150
; TYPE: DNA
; ORGANISM: Pinus radiata
US-09-640-211A-2088

Query Match 15.6%; Score 188; DB 3; Length 1150;
Best Local Similarity 72.1%; Pred. No. 2e-30;
Matches 245; Conservative 0; Mismatches 95; Indels 0; Gaps 0;

QY 79 ATGGGAGGAGCTCCGCTGTCGAGAAAGATGGGGCTCAAGAGGGTCCATGAGACGGCGAG 138
DB 63 ATGGGAGATCTCTCGTCTGTGAAAAAGCTCATACAAACAAAGGGCGTGGACCAAGAA 122
QY 139 GAGGACAAAGTCTCTGTCGCCCATTCACGCGCCAGCGCCACGCAATGGCGCGCTTG 198
DB 123 GAGGACGATGCGCTTCATTCGCCCATTCGAACTCAGGGGAAAGTTGGCGGCTGCTT 182
QY 199 CCCAAGCAAGCCGGGCTGCTGCTTGGCGCAAGAGCTCCGGCTCCGGTGGATCAACTAC 258
DB 183 CCCAAGCCGCGAGGGCTGATGCGCTCGGAAAGAGCTGCAAGGCTCCGATGATMAACTAC 242
QY 259 CTGCGGCGGAGCATCAAGGGGGCACTTCTCCAAGGAGGAGGACACCATCATTCAT 318
DB 243 CTGCGTCTGATCTGAAGCGTGGAACCTTCTCAGAAAGAGACGAACTCGTCATCAAA 302

QY 319 CTCACGAGCTGCTTGGCAACAGGTGTCGCAATTGCGCCAGGTTGCCGGGAGAGAG 378
DB 303 CTCACCTCCCTACTCGGCAACAGTGTCTCTTATTGCAAGGAGATTGCCGGCGAGAG 362
QY 379 GACAAAGATCAAGAACGCTGTGGCACACCACTTCAGA 418
DB 363 GACAAAGATMAAGAACTACTGGAATACTACATCAAGA 402

RESULT 11

US-09-640-211A-2087
; Sequence 2087, Application US/09640211A
; Patent No. 6833446
; GENERAL INFORMATION:
; APPLICANT: Wood, Marion
; APPLICANT: Shenk, Michael A.
; APPLICANT: McGrath, Annette
; TITLE OF INVENTION: Compositions and Methods for the
; FILE REFERENCE: 11000.1021CIU
; CURRENT APPLICATION NUMBER: US/09/640,211A
; CURRENT FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 2368
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2087
; LENGTH: 473
; TYPE: DNA
; ORGANISM: Pinus radiata
US-09-640-211A-2087

Query Match 15.1%; Score 181.6; DB 3; Length 473;
Best Local Similarity 70.9%; Pred. No. 4.2e-29;
Matches 241; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

QY 79 ATGGGAGGAGCTCCGCTGTCGAGAAAGATGGGGCTCAAGAGGGTCCATGAGACGGCGAG 138
DB 40 ATGGGAGATCTCTCGTCTGTGAAAAAGCTCATACAAAGGGCGTGGACCAAGAA 99
QY 139 GAGGACAAAGTCTCTGTCGCCCATTCACGCGCCAGCGCCACGCAATGGCGCGCTTG 198
DB 100 GAAAGACGACCGGCTTATCGCTCAATTCGAGCCACGCGGAAGGGGGCTGCTGCTT 159
QY 199 CCCAAGCAAGCCGGGCTGCTGCTTGGCGCAAGAGCTGCGGCTCCGGTGGATCAACTAC 258
DB 160 CCCAAGCCGCGAGGGCTGCTGAGATGCGCAAGAGCTGCAAGCTGATGATMAACTAC 219
QY 259 CTGCGGCGGAGCATCAAGGGGGCACTTCTCCAAGGAGGAGGACACCATCATTCAT 318
DB 220 CTGCGTCCGATCTGAAGGTGGAAGCTTACCGAAGAAAGAGAGCTCATCACTAA 279
QY 319 CTCACGAGCTGCTTGGCAACAGGTGTCGCAATTGCGCCAGGTTGCCGGGAGAGAG 378
DB 280 CTCACCTCCTGCTTGGCAACAGGTGCTTTAATTGCAAGGAGATTGCCGGACGAGAG 339
QY 379 GACAAAGATCAAGAACGCTGTGGCACACCCACCTCAAGA 418
DB 340 GACAAAGATMAAGAACTACTGGAACACACACATCAAGA 379

RESULT 12

US-09-640-211A-2105
; Sequence 2105, Application US/09640211A
; Patent No. 6833446
; GENERAL INFORMATION:
; APPLICANT: Wood, Marion
; APPLICANT: Shenk, Michael A.
; APPLICANT: McGrath, Annette
; TITLE OF INVENTION: Compositions and Methods for the
; FILE REFERENCE: 11000.1021CIU
; CURRENT APPLICATION NUMBER: US/09/640,211A

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; CURRENT FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 2368
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2105
; LENGTH: 1576
; TYPE: DNA
; ORGANISM: Pinus radiata
US-09-640-211A-2105

Query Match      15.1%; Score 181.6; DB 3; Length 1576;
Best Local Similarity 70.9%; Pred. No. 5.4e-29;
Matches 241; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

QY 79 ATGGGAGGGCTCCGCTGCTGCGAAGATGGGGCTCAAGAGGCTCCATGACGCGGAG 138
DB 40 ATGGGAGATCTCCGCTGCTGCGAAGGCTCATACTAACAAGGGGCTGGAATAACA 99
QY 139 GAGACAAAGTCTCTGCTGCTGCGAATCCAGCGCCAGCGCAATGCGCGGCTG 198
DB 100 GAAGACGACCGCTTATCCCTCACAATTCAGGCCAGGGAGGGGGCTGGCGTTGCTT 159
QY 199 CCCAAGCAAGCCGGGCTGCTGCTGCGCAAGAGCTGCGGCTCCGATCACTAC 258
DB 160 CCCAAGCGCGGAGGCTGCTGAGATCGGCAAGAGCTGCGAATGATGATTAATAC 219
QY 259 CTGGCGCGCGACATCAAGGGGGGCACTTCTCCAGAGAGAGAGACCATCAATCCAT 318
DB 220 CTGGCGCTCCGATCTGAAGGCTGAAGCTTCCAGAAAGAAAGACAGCTCATCATCA 279
QY 319 CTCACAGAGCTGCTTGGCAACAGTGTGCTCCGCAATTCGCCAGGTTGCCGAGAG 378
DB 280 CTCACACTCTTGTTGGCAACAGTGTGCTTTAATTGCAAGGAGATGGCCGAGAGAG 339
QY 379 GACAAAGATCAAGAAAGTGTGGCAACCCCACTCAAG 418
DB 340 GACAAAGATTAAGAAAGTGTGGCAACACACATCAAAA 379

RESULT 13
US-09-640-211A-2075
; Sequence 2075; Application US/09640211A
; Patent No. 6833446
; GENERAL INFORMATION:
; APPLICANT: Wood, Marion
; APPLICANT: Shenk, Michael A.
; APPLICANT: McGrath, Annette
; TITLE OF INVENTION: Compositions and Methods for the
; FILE OF INVENTION: Modification of Gene Transcription
; CURRENT APPLICATION NUMBER: US/09/640,211A
; CURRENT FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 2368
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2075
; LENGTH: 636
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-09-640-211A-2075

Query Match      15.1%; Score 181.2; DB 3; Length 636;
Best Local Similarity 69.5%; Pred. No. 5.4e-29;
Matches 246; Conservative 0; Mismatches 108; Indels 0; Gaps 0;

QY 73 AGCACAATGGGAGGGCTCTCGTGGCCACATCCAGCGCCAGCGCAACTGGGCGC 132
DB 61 AGCACAAGACCGGCAACGCGATGCTGCAAGAGTGGGATTAAGAGAGCCCGTGGAGC 120
QY 133 CCGGAGGAGAGCAAGAGTCTCTCGTGGCCACATCCAGCGCCAGCGCAACTGGGCGC 192
DB 121 CCGAGAGAAAGACGAGGTCTCTCGCAGCTACGTGAGAGAGAGAGCGAGGCGGTGGCG 180
QY 193 GCCCTGCCCAAGCAAGCCGAGGTGCTGCTTGGCGGCAAGAGCTGCGGCTCCGATGATC 252
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DB 181 ACCCTCCGAGACGTGCTGCTCCAGCGCTCGGCAAGAGCTGCGCTCGCTGATG 240
QY 253 AACTACTGCGCGCGGACATCAAGCGGGCAACTTTCACAGAGAGAGAGACACATC 312
DB 241 AACTACTGCGCGCTCGCTGCAAGAGAGCGGAGATGCTCCCGATGAGAGACCTCATC 300
QY 313 ATCCATCTCCAGAGCTGCTTGGCAACAGTGTGCTCGCAATTGGCCGCAAGTTGCCGGG 372
DB 301 CTCGCCCTCCAGCGCTCTTGGAAACAGTGTGTTTGTATGCTGGAAGATCCCGGAGC 360
QY 373 AGGAGGACAAAGAGATCAAGAACTGTGGCACACCCACTTCAMAGAGCGCTC 426
DB 361 CGCACGACAAAGAGATCAAGAACTGTGAAACACCCACTCAGCAAAAAGCTC 414

RESULT 14
US-09-640-211A-1797
; Sequence 1797; Application US/09640211A
; Patent No. 6833446
; GENERAL INFORMATION:
; APPLICANT: Wood, Marion
; APPLICANT: Shenk, Michael A.
; APPLICANT: McGrath, Annette
; APPLICANT: Glenn, Matthew
; TITLE OF INVENTION: Compositions and Methods for the
; FILE OF INVENTION: Modification of Gene Transcription
; CURRENT APPLICATION NUMBER: US/09/640,211A
; CURRENT FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 2368
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1797
; LENGTH: 509
; TYPE: DNA
; ORGANISM: Pinus radiata
US-09-640-211A-1797

Query Match      15.0%; Score 180; DB 3; Length 509;
Best Local Similarity 70.6%; Pred. No. 9.2e-29;
Matches 240; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

QY 79 ATGGGAGGAGCTCCGCTGCTGCGAAGATGGGGCTCAAGAGGCTCAATGACGCGGAG 138
DB 45 ATGGGAGATCTCCGCTGCTGCGAAGAGCTCATATCAAAAGGGGCTGAGCTAAACA 104
QY 139 GAGACAAAGTCTGCTGCTGCCACATCCAGCGCCAGCGCAACTGGCGCGGCTG 198
DB 105 GAAGATGACCGCTTATGCTCACAATTCGAGCCACGCGGAAGGGGCTGGCTCTCTT 164
QY 199 CCCAAGCAAGCGGCTGCTGCTGCGCAAGAGCTGCGGCTCGGATGATCAACTAC 258
DB 165 CCCAAGCGCGGAGGCTGCTGAGTGCAGAGAGCTGACATCGATGATTAACCTAC 224
QY 259 CTGGCGCGCGACATCAAGCGGGCAACTTTCACAGAGAGAGAGAGACACATCATCAT 318
DB 225 CTGGCTCCGATCTGAACGCTGAAGGCTTCAACGAAAGAAAGAGAGCTCATCAAA 284
QY 319 CTCACAGAGCTGCTTGGCAACAGTGTGCTCCGCAATTGCGCCAGAGTTGCCGAGAGAG 378
DB 285 CTCACACTCTTGTTGGCAACAGTGTGCTTTAATTGAGAGGAGATGCCCCGAGAGAG 344
QY 379 GACAAAGATCAAGAAAGTGTGGCACACCCACTCAAGA 418
DB 345 GACAAAGATTAAGAAAGTGTGGAACACACATCAAAA 384

RESULT 15
US-09-640-211A-1982
; Sequence 1982; Application US/09640211A
; Patent No. 6833446
; GENERAL INFORMATION:
; APPLICANT: Wood, Marion
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APPLICANT: Shenk, Michael A.
APPLICANT: McGrath, Annele
APPLICANT: Glenn, Matthew
TITLE OF INVENTION: Compositions and Methods for the
FILE REFERENCE: 11000.1021C1U
CURRENT APPLICATION NUMBER: US/09/640,211A
CURRENT FILING DATE: 2000-08-16
NUMBER OF SEQ ID NOS: 2368
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 1982
LENGTH: 373
TYPE: DNA
ORGANISM: Pinus radiata
US-09-640-211A-1982

Query Match 14.9%; Score 179; DB 3; Length 373;
Best Local Similarity 72.1%; Pred. No. 1.4e-28;
Matches 233; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

QY 79 ATGGGAGGGCTCGTCTGCGGAGAGATGGGCTCAAGAGGCTCATGACGCCGAG 138
DB 51 ATGGGAGAGATCTCCCTGCTGTGAAAAAGCTCATATACAAAGGGGCTGAGACCAAGAA 110
QY 139 GAGGACAGGTCTCGTCCGCCACATCCAGCGCCAGGSCAGGCAACTGGCGCGCCCTG 198
DB 111 GAGGAGATGCGCTCATCGCCCATTCGAACTCAGCGCGAAGGTTGCTGGCGCTGCTT 170
QY 199 CCCAAGCAAGCCGGGCTGCTGCGGCAAGAGCTGCCGCTCCGCTGATCAACTAC 258
DB 171 CCCAAGCGCGGAGGCTGATGCGCTGCGGGAAGAGCTGCAGGCTCCGATGATTAACATC 230
QY 259 CTGGCGCCGAGCATCAAGCGGGCAACTTCTCCAGAGAGAGAGACACCATCATCAT 318
DB 231 CTGGCTCTGATCTGAAGCGTGGAACCTTCTCAGAAAGAACGAACTCATCAAA 290
QY 319 CTCACGAGCTGTTGGCAACAGGTGTCGCAATTGCGCGCAAGTTGCCCGGAGAGAG 378
DB 291 CTCACCTCCCTACTCGGCAACAGTGTCTTATTGCAAGGCAGATTGCCCGGCGGACG 350
QY 379 GACAAAGAGATCAAGAACGTGTG 401
DB 351 GACAAAGAGATAAAGAACTACTG 373

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Job time : 467 secs

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

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Perfect score: 1202

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Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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2: gb_esc3:*
3: gb_esc4:*
4: gb_esc5:*
5: gb_esc6:*
6: gb_esc7:*
7: gb_esc8:*
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12: gb_esc13:*
13: gb_esc14:*
14: gb_esc15:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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4	586.2	48.8	601	5	CF986244 15532rsic
5	583	48.5	594	5	CK014002 32319rsic
6	581.6	48.4	657	2	BI805305 S035C08 S
7	577	48.0	585	5	CK014563 32790rsic
8	567.4	47.2	581	5	CK011009 29726rsic
9	548.4	45.6	550	5	CI166609 CI166609
10	546	45.4	561	5	CF990405 24029rsic
11	532	44.3	550	5	CI261029 CI261029
12	530.2	44.1	585	5	CF966458 10191rsic
13	523.6	43.6	544	5	CF988227 17600rsic
14	497	41.3	509	5	CK008265 33406rsic
15	493	41.0	500	5	CI175768 CI175768
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27	391	32.9	410	3	BP432988
28	385.8	32.1	432	2	BM421359
29	376.2	31.3	847	10	DR814848
30	368.2	30.6	453	2	BM420650
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32	351	29.2	874	10	DV472233
33	350.4	29.2	824	10	DV473866
34	350	29.1	893	10	DR741522
35	340.2	28.3	843	5	CK201334
36	340.2	28.3	1082	10	DR741556
37	339.6	28.3	673	3	BQ837968
38	335	27.9	777	7	BF617565
39	331.6	27.6	681	3	BO763917
40	331	27.5	784	10	DV174489
41	330.2	27.5	840	10	DV858941
42	327.8	27.3	1075	10	DR741858
43	327.4	27.2	329	4	CB000724
44	327.4	27.2	609	2	BG300704
45	327.4	27.2	935	2	BG343209

ALIGNMENTS

RESULT 1
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LOCUS
DEFINITION
OSIRCC018187 Oryza sativa Expressed Library Oryza sativa (indica cultivar-group) genomic, genomic survey sequence.
ACCESSION
CL969261
VERSION
CL969261.1 GI:552393152
KEYWORDS
GSS.
SOURCE
Oryza sativa (indica cultivar-group)
ORGANISM
Oryza sativa (indica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BOP clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (baees 1 to 774)
Ma, L., Wang, J., Chen, C., Liu, X., Su, N., Li, L., Wang, X., Gao, M., Jiao, Y., Sun, N., Zhang, X., Bao, J., Sun, D., Zhao, H., Yuan, L., Wong, G. K. S., Deng, X. W. and Wang, J.
An analysis of transcriptional regulation of the rice genome and its comparison to Arabidopsis
Unpublished (2004)
JOURNAL
Contact: Chen Chen
Department of Bioinformatics
Beijing Institute of Genomics
Chinese Academy of Sciences, Beijing 101300, China
Tel: 86-10-80481559
Fax: 86-10-80488676
Email: chenchen@genomics.org.cn
Rice genomic sequence.
Class: exon-trapped.
FEATURES
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/clone_lib="Oryza sativa Expressed Library"
/note="Oryza sativa exon trapped genomic sequences"

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Best Local Similarity 100.0%; Pred. No. 1.3e-16;
Matches 774; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY	139	GAGGACAAAGTCTCTGTGTGCCACATCCAGGCGCA CGGCGCAATGGCGGCGCTG	198
Db	61	GAGGACAAAGTCTCTGTGTGCCACATCCAGGCGCA CGGCGCAATGGCGGCGCTG	120
OY	199	CCCAAGCAAGCGCGGCTCTGTGTGGCGGCAAGACTGCGGCTTCGGTGGATCTAACTAC	258
Db	121	CCCAAGCAAGCGCGGCTCTGTGTGGCGGCAAGACTGCGGCTTCGGTGGATCTAACTAC	180
OY	259	CTGCGGCGCGGACATCAAGCGGGGSCAACTTCTTCAAGAGAGAGAGAGACACCATCATCAT	318
Db	181	CTGCGGCGCGGACATCAAGCGGGGSCAACTTCTTCAAGAGAGAGAGAGACACCATCATCAT	240
OY	319	CTCCACGAGCTGTCTTGGSCAA CAGGTGTGCCGCAATTCGCCCGCAGGTTGCCCGGAGAG	378
Db	241	CTCCACGAGCTGTCTTGGSCAA CAGGTGTGCCGCAATTCGCCCGCAGGTTGCCCGGAGAG	300
OY	379	GACAAACGAGATCAAGAAAGTGTGGGACACCCACCTCAAGAAAGCGGCTCATATGCCG	438
Db	301	GACAAACGAGATCAAGAAAGTGTGGGACACCCACCTCAAGAAAGCGGCTCATATGCCG	360
OY	439	CAGGCGGATCATGTGTGCCGCGA CCGGCGGCAAGACAAAGACAAAGACCGAGAGCGCGAAG	498
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OY	499	AAGCCAGCCGCGCGCGCGCGCGCGCGCGCGCGCGCTGCGCCGAGCGGCTCGGCTCGTCG	558
Db	421	AAGCCAGCCGCGCGCGCGCGCGCGCGCGCGCGCGCTGCGCCGAGCGGCTCGGCTCGTCG	480
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OY	619	TGCGGCTCCGCTCCGTGTGTGGCGCCAAAGAGAGACTCTTCACTCGGCTTCCGAGAG	678
Db	541	TGCGGCTCCGCTCCGTGTGTGGCGCCAAAGAGAGACTCTTCACTCGGCTTCCGAGAG	600
OY	679	TTCCGATCGACGACAGCTTCTGTGTGGAGAGCGCTGTGATGCGGCTGGA CGGATACGAC	738
Db	601	TTCCGATCGACGACAGCTTCTGTGTGGAGAGCGCTGTGATGCGGCTGGA CGGATACGAC	660
OY	739	GTTGTCATGAGAGCCCGCGCGAGCGGTTGTCGTGCGGCCCATTCGCGGACGACATGACTAC	798
Db	661	GTTGTCATGAGAGCCCGCGCGAGCGGTTGTCGTGCGGCCCATTCGCGGACGACATGACTAC	720
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Db	721	TGGCTCGAGAGTTCATGAGAGTCGGGCGAAGCGCAAGCTTGCGCGCAGATCTAG	774
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DEFINITION	AB118162 ZAPR1 rice Oc cDNA Oryza sativa (indica cultivar-group)		linear EST 30-NOV-2004
ACCESSION	AB118162		
VERSION	AB118162.1		GI:45244940
KEYWORDS	EST.		
SOURCE	Oryza sativa (indica cultivar-group)		
ORGANISM	Oryza sativa (indica cultivar-group)		
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Bep clade; Ehrhartoideae; Oryzae; Oryza.		
	1 (bases 1 to 638)		
	Fujiwara,S., Tanaka,N., Kaneda,T., Takayama,S., Che,F. and Isozaki,A.		
	Analysis of flagellin perception signaling and role of flagellin in rice immune system using cDNA microarray		
	Unpublished (2004)		
JOURNAL	Comment		
	Contact: Fang-Sik Che		

FEATURES
SOURCE

Graduate School of Biological Sciences
Nara Institute of Science and Technology
816-5, Ikoma-shi, Takayama-chou, Nara 630-0101, Japan
Tel: 81-743-72-5452
Fax: 81-743-72-5459
Email: fscie@b.ist.nara.ac.jp, URL: <http://bsw3.ist.nara.ac.jp>
Location/Qualifiers
1. 638

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/db_xref="taxon:39946"
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/cell_type="suspension culture"
/cell_line="Oc"
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/notes="specimen_voucher: Oc-MA-2002 (NAIST, Japan);
country: Japan; induced by incompatible N161 strain of
Acidovorax avenae"

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ORIGIN

Query Match	52.8%	Score 635;	DB 1;	Length 638;
Best Local Similarity	100.0%	Pred. No. 6.8e-143;		
Matches 635; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0

OY	1	AAGCCGCTCCCTTCCAAAGAACACACACACGCAAGAGAGACAGAGAGATTCAATCAAGC	60
Db	4	CAGCCGCTCCCTTCCAAAGAACACACACACGCAAGAGAGAGAGAGATTCAATCAAGAC	63
OY	61	AGGGAAGAGACAGACACATGGGGAGGGCTCCGTCTCGAAGATGGGGCTCAAGAG	120
Db	64	AGGGAAGAGACACACATGGGGAGGGCTCCGTCTCGAAGATGGGGCTCAAGAG	123
OY	121	GGTCCATGAGACCCGGAGAGAGACAAAGTCTCTGTGCCCAATCCAGGCCACCGGCAC	180
Db	124	GGTCCATGAGACCCGGAGAGAGACAAAGTCTCTGTGCCCAATCCAGGCCACCGGCAC	183
OY	181	GGCAACTGGCGGCGCTGCCCAAGCAACCGGAGCTGTGCGTTGCGGCAAGAGCTGCCG	240
Db	184	GGCAACTGGCGGCGCTGCCCAAGCAACCGGAGCTGTGCGTTGCGGCAAGAGCTGCCG	243
OY	241	CTCGGTGATCAACTACCTGCGGCGGACATCAAGCGGGCACTTCTTCAAGAGAG	300
Db	244	CTCGGTGATCAACTACCTGCGGCGGACATCAAGCGGGCACTTCTTCAAGAGAGAG	303
OY	301	GAGACACCATCATCTCTCCACGAGGTGCTTGGCAACAGGTGGTCCGCAATTGGCGGC	360
Db	304	GAGACACCATCATCTCTCCACGAGGTGCTTGGCAACAGGTGGTCCGCAATTGGCGGC	363
OY	361	AGTTTGCCTGGGAGAGACGCAACAGAGATCAAGAACTGTGGCAACCCACTCAAGAG	420
Db	364	AGTTTGCCTGGGAGAGACGCAACAGAGATCAAGAACTGTGGCAACCCACTCAAGAG	423
OY	421	CGCTTCGATGCGCGGCTCAGGGCGGTATGTCTGGGCGAGGGGCGGCAAGAAAGCAAG	480
Db	424	CGCTTCGATGCGCGGCTCAGGGCGGTATGTCTGGGCGAGGGGCGGCAAGAAAGCAAG	483
OY	481	AAGCGGAAGACGGCAAGAGCAACCGCGCGCGCGCGCGCGCGCGCGCTGCGCCGAG	540
Db	484	AAGCGGAAGACGGCAAGAGCAACCGCGCGCGCGCGCGCGCGCGCGCTGCGCCGAG	543
OY	541	CGGTCCGCTCGTGTGCGTGAACGAGTCTTCGATGGCTCGTGTGCGGAGAGAGCAAC	600
Db	544	CGGTCCGCTCGTGTGCGTGAACGAGTCTTCGATGGCTCGTGTGCGGAGAGAGAGCAAC	603
OY	601	GGCAACGCGGGAGATCACTCGGCGTCCGCGTCCGT 635	
Db	604	GGCAACGCGGGAGATCACTCGGCGTCCGCGTCCGT 638	

RESULT 3			
CK008102			
LOCUS	621 bp	mRNA	linear
CK008102			EST 04-FEB-2005

DEFINITION	279533ricef_4052.y1 Oryza sativa cv. Pa64s panicle sterile cDNA library Oryza sativa (indica cultivar-group) cDNA 5', mRNA sequence.
ACCESSION	CK008102
VERSION	CK008102.1
KEYWORDS	GI:58597574
SOURCE	EST.
ORGANISM	Oryza sativa (indica cultivar-group)
REFERENCE	Oryza sativa (indica cultivar-group)
AUTHORS	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.
	1 (bases 1 to 621)
	Hu, J., Wang, J., Lin, W., Li, S., Li, H., Zhou, J., Ni, P., Dong, W., Xu, S., Zeng, C., Zhang, J., Zhang, Y., Li, R., Xu, Z., Li, S., Li, X., Zheng, H., Gong, L., Lin, L., Yin, J., Geng, J., Li, G., Shi, J., Liu, J., Lv, H., Li, J., Wang, J., Deng, Y., Ran, L., Shi, X., Wang, X., Wu, Q., Li, C., Ren, X., Wang, J., Wang, X., Li, D., Liu, D., Zhang, X., Ji, Z., Zhao, W., Sun, Y., Zhang, Z., Bao, J., Han, Y., Dong, L., Ji, T., Chen, P., Wu, S. and Liu, J.
TITLE	The Genomes of Oryza sativa: A History of Duplications
JOURNAL	PLoS Biol. 3 (2), e38 (2005)
PUBMED	15685292
COMMENT	Contact: Yan Zhou Bioinformatics Department Hangzhou Genomics Institute No. 51 Zhijiang Road, Hangzhou 310008, China Tel: 86-571-56805886 Fax: 86-571-56805884 Email: zhouyan@genomics.org.cn Seq primer: M13 Forward High quality sequence stop: 621 POLYA=No
FEATURES	Location/Qualifiers
Source	1..621
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	/dev_stage="heading/flowering"
	/clone_lib="Oryza sativa cv. Pa64s panicle sterile cDNA library"
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	Query Match 50.6%; Score 608.4; DB 5; Length 621;
	Best Local Similarity 99.8%; Pred. No. 1.9e-136;
	Matches 609; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy	527 CGGCGTCCCGCGAGCGTCCGCTGCTGCTGCGTGCAGGAGTCCATGAGTGGCTGCTCGG 586
Db	12 CGGCGTCCCGCGAGCGTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 71
Oy	587 TGGCGAGAGACACGCGCAACCGCCGGATCACTCGCGCTCCGCGTCCGCTGCTGCGCAAG 646
Db	72 TGGCGAGAGACACGCGCAACCGCCGGATCACTCGCGCTCCGCGTCCGCTGCTGCGCAAG 131
Oy	647 AGGAGAGTCTCTTACCTCTGCTGCTCCGAGAGTTTCAATGACGACAGCTTTTGGTGG 706
Db	132 AGGAGAGTCTCTTACCTCTGCTGCTCCGAGAGTTTCAATGACGACAGCTTTTGGTGG 191
Oy	707 AGAGCTCTCATGCGCGCTGAGCGGGTACGAGTGTGATGAGAGCCGGCGACGCGCTTG 766
Db	192 AGAGCTCTCATGCGCGCTGAGCGGGTACGAGTGTGATGAGAGCCGGCGACGCGCTTG 251
Oy	767 TCGCGCGCCATTCGCGCGACGACATGACCTACTGCTCGAGTGTTCATGAGATCCGGCG 826
Db	252 TCGCGCGCCATTCGCGCGACGACATGACCTACTGCTCGAGTGTTCATGAGATCCGGCG 311
Oy	827 AAGCGCAAGACTTGGCGCGACATCTTAAAGAAAGAGAAATTTTACGTTTCTTCGCGTTA 886
Db	312 AAGCGCAAGACTTGGCGCGACATCTTAAAGAAAGAGAAATTTTACGTTTCTTCGCGTTA 371

OY		887	ATTGATTTGGTTTTTCTCTCCTCGGCCGCAGCATCTTGACCCGGAAGGACATGTACTTAACGAC	946
Dd		372	ATTGATTTGGTTTTTCTCTCCTCGGCCGCAGCATCTTGACCCGGAAGGACATGTACTTAACGAC	431
OY		947	AAGAGTGTCCATGAGCCAAATCATCAACAAGAGAAGAACGCCAATATCGATGCGATGCGCA	1006
Dd		432	AAGAGTGTCCATGAGCCAAATCATCAACAAGAGAAGAACGCCAATATCGATGCGATGCGCA	491
OY		1007	TGAGATGCACCAGCATGCTTGGATAGTTAATTTTCCTTTTTCCTTCTCTGATGTA	1066
Dd		492	TGAGATGCACCAGCATGCTTGGATAGTTAATTTTCCTTTTTCCTTCTCTGATGTA	551
OY		1067	TAGAAAACGAAGAAGATCAGTATCGAAACCTCGAATCCTTTCTCAATATGTGCAAATCG	1126
Dd		552	TAGAAAACGAAGAAGATCAGTATCGAAACCTCGAATCCTTTCTCAATATGTGCAAATCG	611
OY		1127	ATCATCAGAA	1136
Dd		612	ATCATCAGAA	621
RESULT 4				
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LOCUS				
DEFINITION		601 bp	mRNA	linear EST 04-FEB-2005
		15332stficee_11417.v1	Oryza sativa cv. LYP9 cllering whole plant	
		CNDA library Oryza sativa (indica cultivar-group)	CNDA 5', mRNA	
		sequence.		
ACCESSION		CP986244		
VERSION		CP986244.1	GI:58587936	
KEYWORDS		EST.		
SOURCE		Oryza sativa (indica cultivar-group)		
ORGANISM		Oryza sativa (indica cultivar-group)		
		Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
		Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP		
		clade; Ehrhartioideae; Oryzaceae; Oryza.		
REFERENCE		1 (bases 1 to 601)		
AUTHORS		Yu,J., Wang,J., Lin,W., Li,S., Li,H., Zhou,J., Ni,P., Dong,W., Hu,S., Zeng,C., Zhang,J., Zhang,Y., Li,R., Xu,Z., Li,S., Li,X., Zheng,H., Cong,L., Lin,L., Yin,D., Geng,J., Li,G., Shi,J., Liu,J., Lv,H., Li,J., Wang,J., Deng,Y., Ran,L., Shi,X., Wang,X., Wu,Q., Li,C., Ren,X., Wang,J., Wang,X., Li,D., Liu,D., Zhang,X., Ji,Z., Zhao,W., Sun,Y., Zhang,Z., Bao,D., Han,Y., Dong,L., Ji,J., Chen,P., Wu,S. and Liu,J.		
TITLE		The Genomes of Oryza sativa: A History of Duplications		
JOURNAL		PLOS Biol. 3 (2), e38 (2005)		
PUBMED		15685292		
COMMENT		Contact: Yan Zhou Bioinformatics Department Hangzhou Genomics Institute No.51 ZhiJiang Road, Hangzhou 310008, China Tel: 86-571-56805886 Fax: 86-571-56805884 Email: zhouyan@genomics.org.cn Seq primer: M13 Forward High quality sequence stop: 601 POLYA=No.		
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		CNDA library"		
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Query Match		48.8%; Score 586.2; DB 5; Length 601;		
Best Local Similarity		99.5%; Pred. No. 4,7e-11;		
Matches 588; Conservative		0; Mismatches 3; Indels 0; Gaps 0;		
OY		24 CACAACGCAAGAGAGACAGACTTTCAGATCAGAGACGAGAGAGACAAACACATGGG		83

Db	Accession	Version	KeyWords	Source	Organism	Reference	Authors
Db	11	CACAAACGCAAGGAGGACAGAGAGTTCAAGTTCAGACGACGAGGAGAGCAAGCAACAAAGGAG	70				
Qy	84	GAGGGCTCCGTGCTCCAGAGAGATGGGGCTCAAGAGAGGTCCATGAGACGCCGAGAGAGAGA	143				
Db	71	GAGGGCTCCGTGCTCCAGAGAGATGGGGCTCAAGAGAGGTCCATGAGACGCCGAGAGAGAGA	130				
Qy	144	CAAGTCTCTGCTCCGCCATATCAAGCGGACCGGACCGGCAACTGGCGCTTCGCCCA	203				
Db	131	CAAGTCTCTGCTCCGCCATATCAAGCGGACCGGACCGGCAACTGGCGCTTCGCCCA	190				
Qy	204	GCAAGCCGGGCTGCTGCTCCGTCGGCAGAGCTGCCCTCCGGTGGATCAACTACTCTCG	263				
Db	191	GCAAGCCGGGCTGCTGCTCCGTCGGCAGAGCTGCCCTCCGGTGGATCAACTACTCTCG	250				
Qy	264	GCCGAGCATCAAGCGGGGCAACTTCCAGAGAGAGAGAGACATCATCATCTCTCA	323				
Db	251	GCCGAGCATCAAGCGGGGCAACTTCCAGAGAGAGAGAGACATCATCATCTCTCA	310				
Qy	324	CGAGCTGCTTGGCAACAGTGGTCCGCAATTGCCGACAGTTGCCCGGAGAGACGACAA	383				
Db	311	CGAGCTGCTTGGCAACAGTGGTCCGCAATTGCCGACAGTTGCCCGGAGAGACGACAA	370				
Qy	384	CGAGTCAAGAACGTGTGGACACACCCACTCAAGAGGCTTCATATGGCCGGCTCAAGG	443				
Db	371	CGAGTCAAGAACGTGTGGACACACCCACTCAAGAGGCTTCATATGGCCGGCTCAAGG	430				
Qy	444	CGGTATGTCGCGCGGACGCGCGGACAGACACAGAGCGGACGAGACGCGGAGAGACC	503				
Db	431	CGGTATGTCGCGCGGACGCGCGGACAGACACAGAGCGGACGAGACGCGGAGAGACC	490				
Qy	504	AGCCG	563				
Db	491	AGCCG	550				
Qy	564	GGAGTCCCTCAAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	614				
Db	551	GGAGTCCCTCAAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	601				
RESULT 5	CK014002	594 bp	mRNA	linear	EST 04-FEB-2005		
LOCUS	CK014002	3219ntsizef.1546.y1	Oryza sativa cv. PA64s	particle size	linear cDNA		
DEFINITION	CK014002	library	Oryza sativa (indica cultivar-group)	CDNA 5', mRNA	sequence.		
ACCESSION	CK014002	GI:58603474					
VERSION	CK014002						
KEYWORDS							
SOURCE							
ORGANISM							
REFERENCE							
AUTHORS							
TITLE							
JOURNAL							
COMMENT							

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Best Local Similarity	100.0%; Pred. No. 2,8e-130;	
Matches 583;	Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 CAGCCGCTCTCTTCCAAAGACACACACCCAAAGAGACGACCTTACATCAGAC	60
DB	12 CAGCCGCTCTCTTCCAAAGAACACACACCAAGAGAGACGACCTTACATCAGAC	71
QY	61 AGGGAAGGACCAAGCAATGGGGAGGGCTCCGTCGCGAGAAATGGGGCTCAAGAG	120
DB	72 AGGGAAGGACCAAGCAATGGGAGGGCTCCGTCGCGAGAAATGGGGCTCAAGAG	131
QY	121 GGTCCATGACGCGCGAGAGAGCAAGGTCCTGTCGCCATCCACGCGCAC	180
DB	132 GGTCCATGACGCGCGAGAGAGCAAGGTCCTGTCGCCATCCACGCGCAC	191
QY	181 GGCACCTGGGCGCCCTTGCCCAAGACCGGGCTGTGGCTTGGGCAAGCTGCCG	240
DB	192 GGCACCTGGGCGCCCTTGCCCAAGACCGGGCTGTGGCTTGGGCAAGCTGCCG	251
QY	241 CTCGGTGATCAACTCTGCGGCGGACATCAAGCGGGCAACTTCTCAAGAGAGAG	300
DB	252 CTCGGTGATCAACTCTGCGGCGGACATCAAGCGGGCAACTTCTCAAGAGAGAG	311
QY	301 GAGGACACCATCATCTCTTCCACAGAGCTCTTGGCAACAGTGGTCCGATTTGCCGC	360
DB	312 GAGGACACCATCATCTCTTCCACAGAGCTCTTGGCAACAGTGGTCCGATTTGCCGC	371
QY	361 AGGTGGCCGGGAGAGACGACCAAGAGATCAAGACGTGGGACACCCACTCAAGAG	420
DB	372 AGGTGGCCGGGAGAGACGACCAAGAGATCAAGACGTGGGACACCCACTCAAGAG	431
QY	421 CGCTTCGATCGCGCGCTCAGGGCGGTATGTGCGCGAGCGGCGGCAAGACACAG	480
DB	432 CGCTTCGATCGCGCGCTCAGGGCGGTATGTGCGCGAGCGGCGGCAAGACACAG	491
QY	481 AAGCCGAAGCCCGAAGAACCAAGCCGCGCGCGCGCGCGCGCGCGCGCGCGCGAG	540
DB	492 AAGCCGAAGCCCGAAGAACCAAGCCGCGCGCGCGCGCGCGCGCGCGCGCGAG	551
QY	541 CGGTCCGCTCGTGTGCTGAGAGAGTCTTCGATGGCTCTGT	583
DB	552 CGGTCCGCTCGTGTGCTGAGAGAGTCTTCGATGGCTCTGT	594
RESULT 6	657 bp mRNA linear EST 02-OCT-2001	
BI805305	S035C08 Stem library from Oryza sativa (3-5 leaf stage) Oryza	
LOCUS	sativa cDNA clone S035C08, mRNA sequence.	
ACCESSION	BI805305	
VERSION	BI805305.1 GI:15852509	
KEYWORDS	EST.	
SOURCE	Oryza sativa	
ORGANISM	Oryza sativa	
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP	
	Clade; Eriarthroideae; Oryzaceae; Oryza.	

QY 318 TCTCCACGAGCTGCTTGGCAACAGGTGCTCCGCAATTGCCCGCAGTTGCCCGGAGAGAC 377
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Db 489 GAAGCAGCG 548
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RESULT 8 581 bp mRNA linear EST 04-FEB-2005
LOCUS CK011009
DEFINITION 29726refseq_8456.y1 Oryza sativa cv. Pa64s panicle sterile cDNA
library Oryza sativa (indica cultivar-group) cDNA 5', mRNA
sequence.
ACCESSION CK011009
VERSION CK011009.1 GI:58600481
KEYWORDS EST.
SOURCE Oryza sativa (indica cultivar-group)
ORGANISM Oryza sativa (indica cultivar-group)
Buxaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Bsp
clade; Euphorbiaceae; Oryzae; Oryza.
REFERENCE 1 (bases 1 to 581)
AUTHORS Yu, J., Wang, J., Lin, W., Li, S., Li, H., Zhou, J., Ni, P., Dong, W.,
Hu, S., Zeng, C., Zhang, J., Zhang, Y., Li, R., Xu, Z., Li, S., Li, X.,
Zheng, H., Gong, L., Lin, H., Yin, J., Geng, J., Li, G., Shi, J., Liu, J.,
Lv, H., Li, J., Wang, J., Deng, Y., Ran, L., Shi, X., Wang, X., Wu, Q.,
Li, C., Ren, X., Wang, J., Wang, X., Li, D., Liu, D., Zhang, X., Ji, Z.,
Zhao, W., Sun, Y., Zhang, Z., Bao, J., Han, Y., Dong, L., Ji, J., Chen, P.,
Mu, S. and Liu, J.
TITLE The Genomes of Oryza sativa: A History of Duplications
JOURNAL PLoS Biol. 3 (2), e38 (2005)
PUBMED 15685292
COMMENT Contact: Yan Zhou
Bioinformatics Department
Hangzhou Genomics Institute
No. 51 Zhijiang Road, Hangzhou 310008, China
Tel: 86-571-56805886
Fax: 86-571-56805884
Email: zhouyan@genomics.org.cn
Seq primer: M13 Forward
High quality sequence stop: 581
POLYA=No
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Best Local Similarity 99.7%; Pred. No. 1.7e-126;
Matches 579; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 20 AACACACACGAAAG 79
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Db 1 AACACACACGAAAG 60
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Db 61 TGGGTGAG 120
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QY 139 GAGGACAAAGTCTTGTGTGCGCCACATCCAGGCGCCACGCGCCACAGGCAATGCGCGCC 198
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QY 199 CCCAAGCAAGCGGCGCTGTCGTCGCGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 258
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Db 241 CTGCGCGCGGACATCAAG 300
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QY 319 CTCCACGAGCTGCTTGGCAACAGGTGCTCCGCAATTGCCCGCAGGTTGCCCGGAGAGAG 378
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QY 379 GACACGAGATCAAGAAAGTGTGGCACACCCACTCAAGAAAGCCCTCGATGCGCGCGCT 438
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|
|
RESULT 9 550 bp mRNA linear EST 06-FEB-2006
LOCUS C1166609
DEFINITION C1166609 Oryza sativa (japonica cultivar-group) shoot and callus
Oryza sativa (japonica cultivar-group) cDNA clone 031-M064R-D01 3',
mRNA sequence.
ACCESSION C1166609
VERSION C1166609.1 GI:86526403
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Buxaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Bsp
clade; Euphorbiaceae; Oryzae; Oryza.
REFERENCE 1 (bases 1 to 550)
AUTHORS Kikuchi, S.
TITLE Collection and mapping of over 30,000 transcription units by the
rice full-length cDNA project from japonica rice
JOURNAL Unpublished (2006)
COMMENT Contact: Shoshi Kikuchi
Department of Molecular Genetics, Head of Laboratory of Gene
Expression
National Institute of Agricultural Sciences
2-1-2 Kamondai, Tsukuba, Ibaraki 305-8602, Japan
Tel: 81-29-838-7007
Fax: 81-29-838-7007
Email: skikuchi@nias.affrc.go.jp
This EST clone is one of 780k ESTs of Rice full length cDNA Project
URL: http://cna01.dna.affrc.go.jp/cDNA/NIAS_Rice_Full-length_cDNA_Project_Team_Kikuchi_S.,_Sato_K.,_Nagata_T.,_Kawagashira_N.,_Doi_K.,_Kishimoto_N.,_Yazaki_U.,

Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T., Yamamoto, M., and Nakanama, Y.
FAIS Genome Sequencing & Analysis Group: Otsu, Y., Iida, Y., Fujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M., Kodama, T., Kurotaki, T., Kusumegi, T., Lu, M., Masuda, H., Mura, J., Mizuno, K., Naitaka, R., Nishikura, Y., Oka, M., Ryu, R., Sugano, S., Sugiyama, A., Suzuki, Y., Tsuruda, Y., Ueda, M., Xie, Q., Yokomizo, S., Yoshimura, A., Matsubara, K., and Murakami, K.
Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carinici, P., Fukuda, S., Hanagata, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hirooka, T., Hori, F., Iida, J., Imamura, K., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawai, J., Kishikawa-Hirozane, T., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Ootani, N., Ota, Y., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Saeki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takanashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Waki, K., Yasunishi, A., and Hayashizaki, Y.

FEATURES

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1 GTGCGCGAAGAGAGAGCTCTTCACTCGCGCTTCGAGAGCTTCAGATCGACGACAG 60
696 CTTTGTGTGGAGAGCGCTGCTCCATGCGCGCTGAGCGGCTACGAGTGTCCATGAGCGCGG 755
61 CTTTGTGTGGAGAGCGCTGCTCCATGCGCGCTGAGCGGCTACGAGTGTCCATGAGCGCGG 120
756 CGACGGTTCGTCGCGCGCGCATCCGCGACGACATGAGTACTGAGCTCGAGTGTTCAT 815
121 CGACGGTTCGTCGCGCGCGCATCCGCGACGACATGAGTACTGAGCTCGAGTGTTCAT 180
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241 TTCTTGGGTTAATGATTTGTTTCTCTCTGCGCGCATTTTGACCGGAGACAT 300
936 AGCTAAGACAGACAGAGTGTCCATGAGCAGATCATCAAGCAGAAAGCGAATCATGCG 995
301 AGCTAAGACAGACAGAGTGTCCATGAGCAGATCATCAAGCAGAAAGCGAATCATGCG 360
996 ATGCGATGCGATGAGATGACACCCAGTAGCTTTGATAGTTAATTTCTTTTAACTCTCT 1055
361 ATGCGATGCGATGAGATGACACCCAGTAGCTTTGATAGTTAATTTCTTTTAACTCTCT 420
1056 TCTCTGATATATGAAACAGAGATCATGATTCGAAAACCTGAGATCTTTTCTCAAT 1115
421 TCTCTGATATATGAAACAGAGATCATGATTCGAAAACCTGAGATCTTTTCTCAAT 480
1116 GTGCAAACTGATCATCAGAAAACGGGCTCTGCGTTTCTCATTTGATTAATTAATTCAA 1175

DB 481 GTGCAAACTGATCATCAGAAAACGGGCTCTGCGTTTCTCATTTGATTAATTAATTCAA 540
QY 1176 CTTGCAAGCT 1185
DB 541 CTTGCAAGCT 550

RESULT 10

LOCUS CF990405 561 bp mRNA linear EST 04-FEB-2005
DEFINITION 24039srcscee 5646.y1 Oryza sativa cv. LYP9 cillerling whole plant
CDNA library Oryza sativa (indica cultivar-group) cDNA 5', mRNA
sequence.

ACCESSION

CF990405 GI:58592097

VERSION

CF990405.1

SOURCE

ORGANISM

REFERENCE

AUTHORS

Yu, J., Wang, J., Lin, W., Li, S., Li, H., Zhou, J., Ni, P., Dong, W., Hu, S., Zeng, C., Zhang, J., Zhang, Y., Li, R., Xu, Z., Li, S., Li, X., Zheng, H., Cong, L., Lin, L., Yin, J., Geng, J., Li, G., Shi, J., Liu, J., Lv, H., Li, J., Wang, J., Deng, Y., Ran, L., Shi, X., Wang, X., Wu, O., Li, C., Ren, X., Wang, J., Wang, X., Li, D., Liu, D., Zhang, X., Ji, Z., Zhao, W., Sun, Y., Zhang, Z., Bao, J., Han, Y., Dong, L., Ji, J., Chen, P., Wu, S., and Liu, J.
The Genomes of Oryza sativa: A History of Duplications
Plos Biol. 3 (2), e38 (2005)
15685292

COMMENT

Contact: Yan Zhou
Bioinformatics Department
Hangzhou Genomics Institute
No. 51 Zhijiang Road, Hangzhou 310008, China
Tel: 86-571-56805886
Fax: 86-571-56805884
Email: zhouyan@genomics.org.cn
Seq primer: M13 Forward
High quality sequence stop: 561
POLYA=No.

FEATURES

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Best Local Similarity 100.0%; Pred. No. 2.6e-121;
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76 AGGAAAGAGCAAGCAATGGGAGAGGCTCCGTCTGCGAAGATGGGGCTCAAGAG 135
121 GGTCAATGAGCGCGGAGAGAGCAAGTCTCTGTCGCCACATCCAGGCCACGCGCAC 180
136 GGTCAATGAGCGCGGAGAGAGCAAGTCTCTGTCGCCACATCCAGGCCACGCGCAC 195
181 GGTCAATGAGCGCGCGCTGCGCAAGAGCGGAGCTGCTGCGCGCAAGAGCTGCGCG 240
196 GGTCAATGAGCGCGCGCTGCGCAAGAGCGGAGCTGCTGCGCGCAAGAGCTGCGCG 255

QY 241 CTCGGTGGATGAACCTACTGCGCGGCATCAAGCGGGGCACTTCTCCAAAGAGAG 300
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QY 361 AGGTGCCCCGGAGAGCGAGCAACGAGATCAAGAACGTGTGCAACCCCACTCAAGAG 420
Db 376 AGGTGCCCCGGAGAGCGAGCAACGAGATCAAGAACGTGTGCAACCCCACTCAAGAG 435
QY 421 CGCCTCGATGCGCGCGCTGAGGCGGCTCACTGTCGGCGAGGCGGGGCAAGAGCAAG 480
Db 436 CGCCTCGATGCGCGCGCTGAGGCGGCTCACTGTCGGCGAGGCGGGGCAAGAGCAAG 495
QY 481 AAGCCGAAAGGCGGAAAGAGCCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 540
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QY 541 CGGTCC 546
Db 556 CGGTCC 561

RESULT 11

C1261029

LOCUS C1261029 Oryza sativa (japonica cultivar-group) Shoot and root of
DEFINITION germinating seeds Oryza sativa (japonica cultivar-group) cDNA clone
C1261029 550 bp mRNA linear EST 07-FEB-2006
VERSION C1261029.1 GI:86854961

KEYWORDS
SOURCE
ORGANISM

Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BPP
Clade; Ehrhartoideae; Oryzae; Oryza.
1 (bases 1 to 550)
Kikuchi, S.

Collection and mapping of over 30,000 transcription units by the
rice full-length cDNA project from japonica rice
Unpublished (2005)

JOURNAL

COMMENT Department of Molecular Genetics, Head of Laboratory of Gene
Expression

National Institute of Agrobiological Sciences
2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan
Tel: 81-29-838-7007

Fax: 81-29-838-7007

Email: skikuchi@nias.affrc.go.jp

This EST clone is one of 780k ESTs of Rice full length cDNA Project
URL: <http://cdna01.dna.affrc.go.jp/cdna/>

NIAS Rice Full-length cDNA Project Team: Kikuchi, S., Satoh, K.,
Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J.,
Ishikawa, M., Yamada, H., Ooka, H., Horita, I., Kojima, K., Naniki, T.,
Ohneda, E., Yanagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T.,
Yamamoto, M. and Nakahama, Y.

FAIS Genome Sequencing & Analysis Group: Otomo, Y., Iida, Y.,
Fujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M.,
Kodama, T., Kurosaki, R., Kusumegi, T., Lu, M., Maeda, H., Mura, J.,
Mizuno, K., Narikawa, R., Nishikura, J., Oka, M., Ryo, R., Sugano, S.,
Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S.,
Yoshimura, A., Matubara, K. and Murakami, K.

Genome Exploration Research Group in Riken Genomic Sciences Center
and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K.,
Akinura, T., Arakawa, T., Carrinchi, P., Fukuda, S., Hanagaki, T.,
Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K.,
Hirooka, T., Hori, F., Iida, J., Imamura, K., Imocani, K., Ishii, Y.,
Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawai, J.,
Kishikawa-Hirozane, T., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,

Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
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Saeki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T.,
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Yasunishi, A. and Hayashizaki, Y.

FEATURES

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ORIGIN

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QY 754 GCGCAGCGGCTTGTGTGCGCGCGCATCCGCGAGCATGAGTACTGCTCGAGATGTTTC 813
Db 120 GCGCAGCGGCTTGTGTGCGCGCGCATCCGCGAGCATGAGTACTGCTCGAGATGTTTC 179

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Db 540 AACT 543

RESULT 12

CF966458/c

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DEFINITION 10191xiced 10977.y1 Oryza sativa cv. LYP9 trefoil whole plant cDNA
library Oryza sativa (indica cultivar-group) cDNA 5', mRNA
sequence.

ACCESSION CF966458
VERSION CF966458.1 GI:38482419

KEYWORDS
EST.

Source	Organism	Reference Authors	Title	Journal	PubMed	Comment	Features	Source	
Oryza sativa (indica cultivar-group)	Oryza sativa (indica cultivar-group)	Yu, J., Wang, J., Lin, M., Li, S., Li, H., Zhou, J., Ni, P., Dong, W., Hu, S., Zeng, C., Zhang, J., Zhang, Y., Li, R., Xu, Z., Li, S., Li, X., Zheng, H., Gong, L., Lin, L., Yin, J., Geng, J., Li, G., Shi, J., Liu, J., Lv, H., Li, J., Wang, J., Deng, Y., Ran, L., Shi, X., Wang, X., Wu, Q., Li, C., Ren, X., Wang, J., Wang, X., Li, D., Liu, D., Zhang, X., Ji, Z., Zhao, W., Sun, Y., Zhang, Z., Bao, J., Han, Y., Dong, L., Ji, J., Chen, P., Wu, S. and Liu, J.	The Genomes of <i>Oryza sativa</i> : A History of Duplications	PLOS Biol. 3 (2), e38 (2005)	15685292	Contact: Yan Zhou Bioinformatics Department Hangzhou Genomics Institute No. 51 Zhiliang Road, Hangzhou 310008, China Tel: 86-571-56805886 Fax: 86-571-56805884 Email: zhoyuan@genomics.org.cn Seq primer: M13 Forward High quality sequence stop: 585 POLYA=No.	location/Qualifiers 1..585 /organism="Oryza sativa (indica cultivar-group)" /mol_type="rRNA" /cultivar="Lyp9" /db_xref="taxon:39946" /label_type="whole plant" /dev_stage="trefoil1" /clone_idb="Oryza sativa cv. LYP9 trefoil whole plant cDNA library"		
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OY	592	GAGGAGCAGCGGACGCGGGATCAGCTCGGCGTCGCGGTCGCGTCCGTGCGCCAGAGAGAG	651						
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OY	652	AGCTCCTTCACTCGGCTTCCGAGAGTTCCAGATCGACGACAGTTCTGCTCGGAGAG	711						
DB	525	AGCTCCTTCACTCGGCTTCCGAGAGTTCCAGATCGACGACAGTTCTGCTCGGAGAG	466						
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OY	772	CCGCCATCGCGGACGACATGAGTACTGTGCTCGGAGTTCATGAGATCCGGCGAGCG	831						
DB	405	CCGCCATCGCGGACGACATGAGTACTGTGCTCGGAGTTCATGAGATCCGGCGAGCG	346						
OY	832	CAAGACTTGGCGGACATTTAGAGAAAGAGAGAAATTTTACCGTTCTTTCGTTAATTGA	891						
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OY	892	TTTGTCTTCTCTCTGCGGCACTTTGACCGGAGGACATAGTAAACAGACAGAG	951						
DB	285	TTTGTCTTCTCTCTGCGGCACTTTGACCGGAGGACATAGTAAACAGACAGAG	226						
OY	952	TGTCCATGAGCGAATCATCAAGCAGAGAAAGCGCAATCATGCGATGCGATGCGATGAGA	1011						
DB	225	TGTCCATGAGCGAATCATCAAGCAGAGAAAGCGCAATCATGCGATGCGATGCGATGAGA	166						
OY	1012	TGCACCCAGTACTGTGATAGTAAATTTTCTTTTAACTCTCTCCGTATGATATGAA	1071						
DB	165	TGCACCCAGTACTGTGATAGTAAATTTTCTTTTAACTCTCTCCGTATGATATGAA	106						

Oy	1072	ACAAAGAGTACTGATTCGAACCTGAGATCCCTTTCACAAATGTCAAACTGGATCAT	1133
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DEFINITION	176005ricee.15506.y1 Oryza sativa cv. LYP9 clltering whole plant		
CDNA library Oryza sativa (indica cultivar-group) cDNA 5', mRNA			
sequence.			
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VERSION	CF988227.1	GI:58589919	
SOURCE	EST.		
ORGANISM	Oryza sativa (indica cultivar-group)		
REFERENCE	Oryza sativa (indica cultivar-group)		
AUTHORS	Eukaryote, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Bep clade; Ehrhartoideae; Oryzaceae; Oryza.		
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	Yu,J., Wang,J., Lin,W., Li,S., Li,H., Zhou,J., Ni,P., Dong,W., Hu,S., Zeng,C., Zhang,J., Zhang,Y., Li,R., Xu,Z., Li,S., Li,X., Lv,H., Li,J., Wang,J., Deng,X., Ran,L., Shi,X., Wang,X., Wu,Q., Li,C., Ran,X., Wang,J., Wang,X., Li,D., Liu,D., Zhang,X., Ji,Z., Zhao,W., Sun,Y., Zhang,Z., Bao,J., Han,Y., Dong,L., Ji,J., Chen,P., Wu,S. and Liu,Y.		
TITLE	The Genomes of Oryza sativa: A History of Duplications		
JOURNAL	Plos Biol. 3 (2), e38 (2005)		
PUBMED	15685292		
COMMENT	Contact: Yan Zhou Bioinformatics Department Hangzhou Genomics Institute No.51 Zhijiang Road, Hangzhou 310008, China Tel: 86-571-56805886 Fax: 86-571-56805884 Email: zhouyan@genomics.org.cn Seq primer: M13 Forward High quality sequence stop: 544 POLYA=No.		
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Oy	360	CAGTTGCCGGGAGACGACAAAGATCAGAAAGTGTGGGACACACCCACTCAAGAA	419
Db	75	CAGTTGCCGGGAGACGACAAAGATCAGAAAGTGTGGGACACACCCACTCAAGAA	134
Oy	420	GGCGCTCGATGCGCGGAGCTCAGGCGGATGTGGCGCGAGCGCGGCAAGAGACCAA	479
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Ohneda, E., Yahagi, M., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T., Yamamoto, M., and Nakahama, Y.
 FAIS Genome Sequencing & Analysis Group: Otsomo, Y., Iida, Y., Fujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M., Kodama, T., Kurosaki, T., Kusumegi, T., Lu, M., Masuda, H., Miura, J., Mizuno, K., Narikawa, R., Nikiura, J., Oka, M., Ryu, R., Sugano, S., Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S., Yoshimura, A., Matsubara, K., and Murakami, K.
 Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carlini, P., Fukuda, S., Hanagata, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hirooka, T., Hori, F., Iida, J., Imamura, K., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawai, J., Kishikawa-Hirozane, T., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Osato, N., Ota, Y., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Saeki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagami, T., Takeda, Y., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Waki, K., Yasunishi, A., and Hayashizaki, Y.
 Location/Qualifiers

FEATURES

source

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ORIGIN

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 DB 481 ATTAATTCACACT 493

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using bw model

Run on: June 24, 2006, 18:02:33 ; Search time 1453 Seconds
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5767.820 Million cell updates/sec

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Perfect score: 1202
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 2: geneseqn1990s:*
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SUMMARIES

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6	420	34.9	454	10	ADD16949
7	420	34.9	454	10	ADK59612
8	375.2	31.2	1276	13	AD084500
9	375.2	31.2	1352	12	AD142105
10	375.2	31.2	1352	12	AD002648
11	366	30.4	1280	13	AD031537
12	366	30.4	1280	12	AD031537
13	366	30.4	1344	12	AD002644
14	352.6	29.3	1126	13	ADX50163
15	352.6	29.3	1192	12	AD142104
16	352.6	29.3	1492	12	AD002647
17	331.2	27.6	1084	12	AD142103
18	331.2	27.6	1084	12	AD002646

19	326.6	27.2	1074	6	ABT08112	Abt08112 Myb-relat
20	326.6	27.2	1074	12	ADH50099	Adh50099 Rice Myb-
21	315.6	26.3	1083	3	ACG1733	Acg1733 Zea may
22	314.2	26.1	662	12	AD142102	Ad142102 Plant tra
23	314.2	26.1	662	12	AD002645	Ad002645 Corn orth
24	312.6	26.0	1086	13	AD082450	Ad082450 Plant ful
25	307.8	25.6	335	10	ADK56097	Adk56097 Plant DNA
26	302.8	25.2	643	12	AD142100	Ad142100 Plant tra
27	302.8	25.2	643	12	AD002643	Ad002643 Rice orth
28	284.2	23.6	672	8	ADA70307	Ada70307 Rice gene
29	278.8	23.2	577	6	ABT08129	Abt08129 Myb-relat
30	278.8	23.2	577	12	ADH50133	Adh50133 Rice Myb-
31	271.8	22.6	777	12	AD143079	Ad143079 Plant tra
32	271.8	22.6	777	12	AD003223	Ad003223 Corn orth
33	268.8	22.4	834	8	ADA69359	Ada69359 Rice gene
34	245.8	20.4	1023	8	ADA69370	Ada69370 Rice gene
35	244.6	20.3	1285	13	ADK60547	Adk60547 Plant ful
36	244.6	20.3	1302	12	AD143080	Ad143080 Plant tra
37	244.6	20.3	1302	12	AD003224	Ad003224 Corn orth
38	243	20.2	1427	8	ACD07381	AcD07381 Rice Myb-
39	243	20.2	1427	12	ADJ77726	AdJ77726 CDNA enco
40	241.2	20.1	966	14	AEA26884	Aea26884 Stress to
41	236.2	19.7	1540	13	ADT17583	AdT17583 Plant CDN
42	235.8	19.6	1772	13	ADX51623	AdX51623 Plant ful
43	234.6	19.5	664	12	AD141904	Ad141904 Plant CDN
44	234.2	19.5	477	3	ACA11294	AcA11294 Zea may
45	234	19.5	1107	8	ADA70309	Ada70309 Rice gene

ALIGNMENTS

RESULT 1	ADA48105	standard; DNA; 816 BP.
XX	XX	
AC	ADA48105;	
XX	XX	
DT	20-NOV-2003	(first entry)
XX	XX	
DE	Rice gene conferring disease resistance in plants.	
XX	XX	
KW	disease resistance; pathogen tolerance; plant pathogen; ds; gene; plant.	
OS	Oryza sativa.	
XX	XX	
PN	WO2003000906-A2.	
XX	XX	
PD	03-JAN-2003.	
XX	XX	
PF	21-JUN-2002; 2002WO-1B002453.	
XX	XX	
PR	22-JUN-2001; 2001US-0300112P.	
XX	XX	
PR	26-SEP-2001; 2001US-0352277P.	
XX	XX	
PR	22-MAR-2002; 2002US-0366535P.	
XX	XX	
PA	(SYGN) SYNGENTA PARTICIPATIONS AG.	
XX	XX	
PI	Glazebrook J, Briggs S, Cooper B, Goff SA, Moughamer T;	
XX	XX	
PI	Katagiri F, Krepe J, Provart N, Rieke D, Zhu T;	
XX	XX	
DR	WPI, 2003-184052/18.	
XX	XX	
DR	P-PSDB; ADA48106.	
XX	XX	
PT	New polynucleotide comprising a plant nucleotide sequence having an open	
XX	XX	
PT	reading frame that encodes a polypeptide associated with disease	
XX	XX	
PT	resistance, useful for conferring resistance or tolerance to a plant	
XX	XX	
XX	XX	
PS	Claim 1; SEQ ID NO 175; 299pp; English.	
XX	XX	
CC	The invention relates to a novel isolated polynucleotide comprising a	
XX	XX	
CC	plant nucleotide sequence having an open reading frame that encodes a	

CC polypeptide associated with disease resistance or its fragment having
CC substantially the same activity as the full-length polypeptide. The
CC polynucleotide of the invention is useful for conferring resistance or
CC tolerance to a plant pathogen. The present sequence represents a protein
CC conferring disease resistance used in the invention.

SQ Sequence 816 BP; 164 A; 254 C; 280 G; 118 T; 0 U; 0 Other;

Query Match	63.6%	Score 752.6	DB 9	Length 816
Best Local Similarly	98.4%	Pred. No. 2.9e-139		
Matches 804; Conservative	0	Mismatches 4	Indels 9	Gaps 4

Qy	79	ATGGGAGGGGCTCCGCTGCGAGAAAGATGGGGCTCAAGAAAGGCTCATGGACCGCGAG	138
Db	1	ATGGGGAAGGCTCCGCTGCTGCAGAAAGATGGGGCTCAAGAAAGGCTCATGGACCGCGAG	60
Qy	139	GAGGACAAGGTCCTCGTCCGCCACATCCAGCGCCACGGCCACGGCAACTGGCGGCGCTTG	198
Db	61	GAGGACAAGGTCCTCGTCCGCCACATCCAGCGCCACGGCCACGGCAACTGGCGGCGCTTG	120
Qy	199	CCCAACCAAGCC----GGGCTGCTCGTTTGGCGGCAAGAGCTGGCGGCTCCGGTGGATCA	254
Db	121	CCCAACCAAGCCGGGCAAGGCTGCTCGTTGGCGGCAAGAGCTGGCGGCTCCGGTGGATCA	180
Qy	255	CTACTCGCGGCGGACATCAACGGGGCACTTCTCCAGGAGGAGGAGGACACATCAT	314
Db	181	CTACTCGCGGCGGACATCAACGGGGCACTTCTCCAGGAGGAGGAGGACACATCAT	240
Qy	315	CCATCTCCACGAGCTGCTTGGCA--CAGTGGTCGCAATTGCCCGCAGGTTGCCCG	371
Db	241	CCATCTCCACGAGCTGCTTGGCAAGCAGGTTGGTCGCCCAATTGCCCGCAGGTTGCCCG	300
Qy	372	GAGGAGGGAACAACGATCAAGAAGTGTGGAC-ACCACCTCAAGAAAGGCGCTGATG	430
Db	301	GAGGAGGGAACAAGGATCAAGAAAGTGTGGACACCACCTCAAGAAAGGCGCTGATG	360
Qy	431	CGCGGCTCAGGGCGGTCATGTCTGGGCGAGCGGCGGCAAGACACAAAGGCCGAAGA	490
Db	361	CGCGGCTCAGGGCGGTCATGTCTGGGCGAGCGGCGGCAAGACACAAAGGCCGAAGA	420
Qy	491	GCGCGAAGAACCCAGCGCGCGCGCGCGCGCGCGCGCTCGCGGAGCGGTCCGCT	550
Db	421	GCGCGAAGAACCCAGCGCGCGCGCGCGCGCG-GCCCGCGGCTCCCGCGAGGCGTCCGCT	479
Qy	551	CGTCGTCCGATGACGAGGCTCTCGATGAGGCTCGTCCGTGGCGGAGAGACAGCGCAACGCG	610
Db	480	CGTCGTCCGATGACGAGGCTCTCGATGAGGCTCGTCCGTGGCGGAGAGACAGCGCAACGCG	539
Qy	611	GGATCAGCTCGGCGTCCGCGTCCGTGTGCGCCAAAGAGAGGCTCCTTCACTCGGCTT	670
Db	540	GGATCAGCTCGGCGTCCGCGTCCGTGTGCGCCAAAGAGAGGCTCCTTCACTCGGCTT	599
Qy	671	CCGAGGAGTTCCAGATCGACGACGAGCTTGTGGTCCGAGACGCTGTGATGCGCTGGACG	730
Db	600	CCGAGGAGTTCCAGATCGACGAGCTTGTGGTCCGAGACGCTGTGATGCGCTGGACG	659
Qy	731	GGAACAGCGTGTCAATGAGAGCCCGGCGACGGTTGATGGCGCGGCATCCGCGGACGACA	790
Db	660	GGAACAGCGTGTCAATGAGAGCCCGGCGAGGCTTGTGTCGCGCGGCATCCGCGGACGACA	719
Qy	791	TGGACTACTGGCTCGAGTGTTCATGAGTCCGGCGGAACGCGCAAGCTTGCAGATCT	850
Db	720	TGGACTACTGGCTCGAGTGTTCATGAGTCCGGCGGAACGCGCAAGCTTGCAGATCT	779
Qy	851	AGAGAAAGAGAGAAATTTTACCCTTTCTTCGCTTAA	887
Db	780	AGAGAAAGAGAGAAATTTTACCCTTTCTTCGCTTAA	816

RESULT 2
ACL26123
ID ACL26123 standard; cDNA; 816 BP.
XX

AC ACU26123;
XX 02-JUN-2005 (first entry)
XX
XX Rice abiotic stress responsive polynucleotide SEQ ID NO:79.
DE
XX ss; abiotic stress tolerance; transgenic plant; plant; cereal;
KW agriculture.
KW
XX Oryza sativa.
OS
XX WO2003008540-A2.
PN
XX 30-JAN-2003.
XX
XX 21-JUN-2002; 2002WO-US019668.
XX
XX 22-JUN-2001; 2001US-0300112P.
PR 24-AUG-2001; 2001US-0314662P.
PR 26-SEP-2001; 2001US-0325277P.
PR 21-NOV-2001; 2001US-03321332P.
XX
XX (SYGN) SYNGENTA PARTICIPATIONS AG.
PA
XX Kreps J, Briggs SP, Cooper B, Glarebrook J, Goff SA, Katagiri F;
PI Moughamer T, Provart N, Rieke D, Zhu T;
XX
XX WPI; 2003-248011/24.
DR
XX New stress-responsive nucleic acid, useful for altering the
PT responsiveness of a plant, e.g. cereal, to an abiotic stress such as cold
PT stress, salt stress or osmotic stress.
PT
XX
XX Claim 1; SEQ ID NO 79; 89pp; English.
PS
XX The invention relates to novel abiotic stress responsive polynucleotides
CC and polypeptides. Also disclosed are vectors, expression cassettes, host
CC cells, and plants containing such polynucleotides. Also disclosed are
CC methods for using the polynucleotides and polypeptides to alter the
CC responsiveness of a plant to abiotic stress. The invention is useful in
CC agriculture. The nucleic acid is useful for determining whether a test
CC plant has been exposed to an abiotic stress condition. It is also useful
CC for selecting an agent that alters abiotic stress regulated
CC polynucleotide expression in a plant cell, and to identify a homolog or
CC ortholog to an abiotic stress responsive polynucleotide. The nucleic acid
CC molecule and the polypeptide encoded by it are useful in altering the
CC responsiveness of a plant to an abiotic stress, such as cold stress, salt
CC stress, osmotic stress or any of their combinations. The present sequence
CC is used in the exemplification of the invention
XX
XX Sequence 816 BP; 164 A; 254 C; 280 G; 118 T; 0 U; 0 Other;

Query Match	62.6%	Score 752.6	DB 11	Length 816
Best Local Similarity	98.4%	Pred. No. 2.9e-139		
Matches 804; Conservative	0	Mismatches 14	Indels 9	Gaps 4

Qy	139	GAGGACAAGTCTTGTCGCCCATCCAGCGCCACGCGCACTGGCGCGCTTG	198
Qy	79	TTGGGAGAGGCTCCGCTGCTGCAGAAATGGGGCTCAAGAAAGGCTCATATGACCGCCGGAG	138
Db	1	ATGGGGAAGGCTCCGCTGCTGCAGAAATGGGGCTCAAGAAAGGCTCATATGACCGCGAG	60
Qy	139	GAGGACAAGTCTTGTCGCCCATCCAGCGCCACGCGCACTGGCGCGCTTG	198
Db	61	GAGGACAAGTCTTGTCGCCCATCCAGCGCCACGCGCACTGGCGCGCTTG	120
Qy	199	CCCAAGCAAGC---GGGCTGCTGCTTGGCGCAAGAGCTGCCGCTCCGGTGAATCAA	254
Db	121	CCCAAGCAAGCGGCGAGGGCTGCTGCTTGGCGCAAGAGCTGCCGCTCCGGTGAATCAA	180
Qy	255	CTACTCGGCGCGGACATCAAGCGGGGCAACTTCTCAAGAGAGAGACACCATCAT	314
Db	181	CTACTCGGCGCGGACATCAAGCGGGGCAACTTCTCAAGAGAGAGAGACACCATCAT	240
Qy	315	CCATCTCACAGAGCTTGGCAA---CAGGTGTCGCGCAATTGCGCCAGGTTCGCCG	371

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DB 241 CCATCTCCACGAGCTCTTGGCAACAGAGTGTGTCCGCAATTGCCGACAGTTCCCCGG 300
QY 372 GAGGACGCAACAGAGATCAAGAACGTGTGGCAC-ACCCACTCAAGAGCGCTGGATG 430
DB 301 GAGGACGCAACAGAGATCAAGAACGTGTGGCAC-ACCCACTCAAGAGCGCTGGATG 360
QY 431 CCGCGGCTAGGGCGGTCAATGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 490
DB 361 CCGCGGCTAGGGCGGTCAATGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 420
QY 491 GCGCGAAGAGCCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 550
DB 421 GCGCGAAGAGCCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 479
QY 551 CCGTCTCGGTGACGAGAGTCTTGATGGCTCTGTGGTGGCGGAGAGCAGCGGACGCGCG 610
DB 480 CCGTCTCGGTGACGAGAGTCTTGATGGCTCTGTGGTGGCGGAGAGCAGCGGACGCGCG 539
QY 611 GGATCAGCTCGGCGTCCGCGTCCGCTGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 670
DB 540 GGATCAGCTCGGCGTCCGCGTCCGCTGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 599
QY 671 CCGAGAGTTCAGATCGACAGAGCTTCTGTGCGGAGAGCTGTGATGCGCGTGGAGCG 730
DB 600 CCGAGAGTTCAGATCGACAGAGCTTCTGTGCGGAGAGCTGTGATGCGCGTGGAGCG 659
QY 731 GGATCAGCTGTGTCATGAGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 790
DB 660 GGATCAGCTGTGTCATGAGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 719
QY 791 TGGACTACTGCGTCCGAGTTCATGAGAGTCCGCGGCGGCGGCGGCGGCGGCGGCGGCT 850
DB 720 TGGACTACTGCGTCCGAGTTCATGAGAGTCCGCGGCGGCGGCGGCGGCGGCGGCGGCT 779
QY 851 AGAGAAAGAGAGAGAAATTTTACCGTTCTTCGCTTAA 887
DB 780 AGAGAAAGAGAGAGAAATTTTACCGTTCTTCGCTTAA 816

RESULT 3
ADA69954
ID ADA69954 standard; DNA; 774 BP.
XX
AC ADA69954;
XX
DT 20-NOV-2003 (first entry)
XX
DE Rice gene, SEQ ID 3277.
XX
KW plant; bacterial infection; fungal infection; viral infection; rice;
KW gene; db.
XX
OS Oryza sativa.
XX
OS WO2003000898-A1.
XX
PD 03-JAN-2003.
XX
PF 22-JUN-2001; 2001WO-1B001105.
XX
PR 22-JUN-2001; 2001WO-1B001105.
XX
PA (SYGN ) SYNGENTA PARTICIPATIONS AG.
XX
PI Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;
PI Katagiri F, Quan S, Tao Y, Whitman S, Xie Z, Zhu T, Zou G;
XX
DR MPI, 2003-175290/17.
XX
PT Identifying at least one gene involved in plant resistance or response to
PT pathogenic infection for conferring resistance or tolerance to a plant to
PT bacterial, fungal or viral infection by determining or detecting plant

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PT gene expression.
XX
PS Claim 6; SEQ ID NO 3277; 899bp; English.
XX
CC The present invention relates to a method (M1) for identifying genes
CC involved in plant resistance or response to pathogenic infection. M1
CC comprises identifying a gene whose expression is significantly altered in
CC the incompatible interaction of plant gene expression relative to
CC expression of the gene in an uninfected plant, in a mutant plant that
CC does not express a gene associated with response to pathogenic infection,
CC or in a corresponding incompatible or compatible interaction. (M1) is
CC useful for conferring resistance to resistance or tolerance to a plant to
CC bacterial, fungal or viral infection. The present sequence was used to
CC illustrate the invention.
XX
SQ Sequence 774 BP; 150 A; 248 C; 269 G; 107 T; 0 U; 0 Other;
XX
Query Match 61.9%; Score 744.6; DB 8; Length 774;
Best Local Similarity 99.2%; Pred. No. 1,1e-137;
Matches 769; Conservative 0; Mismatches 4; Indels 2; Gaps 2;
QY 79 ATGGGGAAGGCTCCGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 138
DB 1 ATGGGGAAGGCTCCGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 60
QY 139 GAGGACAAAGTCTCTGCTCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 198
DB 61 GAGGACAAAGTCTCTGCTCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 120
QY 199 CCCAAGCAAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 258
DB 121 CCCAAGCAAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 180
QY 259 CTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 318
DB 181 CTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 240
QY 319 CTCCACGAGCTCTTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 378
DB 241 CTCCACGAGCTCTTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 300
QY 379 GACAAAGAGATCAAGAACGCTGTGGCAC-ACCCACTCAAGAGCGCTGGATGCGCGGCG 437
DB 301 GACAAAGAGATCAAGAACGCTGTGGCAC-ACCCACTCAAGAGCGCTGGATGCGCGGCG 360
QY 438 TCAAGGCGGCTCATGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 497
DB 361 TCAAGGCGGCTCATGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 420
QY 498 GAAAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 557
DB 421 GAAAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 479
QY 558 GGTGACGAGTCTTCGATGGCTCTGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 617
DB 480 GGTGACGAGTCTTCGATGGCTCTGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 539
QY 618 CTGCGGCTCGGCTCCGCTGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 677
DB 540 CTGCGGCTCGGCTCCGCTGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 599
QY 678 GTTCCAGATCGACAGAGCTTCTGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 737
DB 600 GTTCCAGATCGACAGAGCTTCTGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 659
QY 738 CGTGTCATGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 797
DB 660 CGTGTCATGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 719
QY 798 CTGACTCGAGTGTTCATGAGAGTCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 852
DB 720 CTGACTCGAGTGTTCATGAGAGTCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 774

```

RESULT 4
ADA48651
ID ADA48651 standard; DNA; 774 BP.
XX
AC ADA48651;
XX
DT 20-NOV-2003 (first entry)
XX
DE Rice gene conferring disease resistance in plants.
XX
KW disease resistance; pathogen tolerance; plant pathogen; ds; gene; plant.
XX
OS Oryza sativa.
XX
PN WO2003000906-A2.
XX
PD 03-JAN-2003.
XX
PF 21-JUN-2002; 2002WO-1B002453.
XX
PR 22-JUN-2001; 2001US-0300112P.
PR 26-SEP-2001; 2001US-0352277P.
PR 22-MAR-2002; 2002US-0366535P.
XX
XX (SYGN) SYNGENTA PARTICIPATIONS AG.
PA Glazebrook J, Briggs S, Cooper B, Goff SA, Moughamer T;
PI Katagiri F, Krepe J, Provart N, Rieke D, Zhu T;
PI MPI: 2003-184052/18.
XX P-PSDB; ADA48652.
DR
XX
PT New polynucleotide comprising a plant nucleotide sequence having an open
PT reading frame that encodes a polypeptide associated with disease
PT resistance, useful for conferring resistance or tolerance to a plant
PT pathogen.
XX
XX Claim 1; SEQ ID NO 721; 299pp; English.
XX
CC The invention relates to a novel isolated polynucleotide comprising a
CC plant nucleotide sequence having an open reading frame that encodes a
CC polypeptide associated with disease resistance or its fragment having
CC substantially the same activity as the full-length polypeptide. The
CC polynucleotide of the invention is useful for conferring resistance or
CC tolerance to a plant pathogen. The present sequence represents a gene
CC conferring disease resistance used in the invention.
XX
XX Sequence 774 BP; 150 A; 248 C; 269 G; 107 T; 0 U; 0 Other;
SO
Query Match 61.9%; Score 744.6; DB 9; Length 774;
Best Local Similarity 99.2%; Pred. No. 1.1e-137;
Matches 769; Conservative 0; Mismatches 4; Indels 2; Gaps 2;
QY 79 ATGGGGAGGGGCTCGGCTGCGAGAGATGGGCTCAAGAGAGGATCATGAGCCGAG 138
DB 1 ATGGGGAAGGCTCGGCTGCGAGAGATGGGCTCAAGAGAGGATCATGAGCCGAG 60
QY 139 GAGGACAGAGTCTCGTCCGCCATCCAGCGCCACGCGCAATGGCGCGCTTG 198
DB 61 GAGGACAGAGTCTCGTCCGCCATCCAGCGCCACGCGCAATGGCGCGCTTG 120
QY 199 CCCAGCAAGCCGGGCTGCTGCGCTTGGCGCAAGCTGCCCGGTCGGGTGATCACTAC 258
DB 121 CCCAGCAAGCCGGGCTGCTGCGCTTGGCGCAAGCTGCCCGGTCGGGTGATCACTAC 180
QY 259 CTGCGCGCGGACATCAAGCGGGGCAACTTCTCCAGGAGAGGAGACATCATCAT 318
DB 181 CTGCGCGCGGACATCAAGCGGGGCAACTTCTCCAGGAGAGGAGACATCATCAT 240
QY 319 CTTCACAGAGCTGTTGGCAACAGGTGATCGCAATTGCCGCCAGTTGCCGGAGAGCG 378
DB 241 CTTCACAGAGCTGTTGGCAACAGGTGATCGCAATTGCCGCCAGTTGCCGGAGAGCG 300

QY 379 GACAAAGAGATCAAGAAAGTGTGGAC-ACCCACCTCAAGAGCGCTCGATGCCCGGC 437
DB 301 GACAAAGAGATCAAGAAAGTGTGGACAAACCACTTCAAGAGCGCTCGATGCCCGGC 360
QY 438 TCAGGCGCGATATGTCGCGGAGCGGCGGCAAGAGCAAGAAAGCGAAGCGCGA 497
DB 361 TCAGGCGCGATATGTCGCGGAGCGGCGGCAAGAGCAAGAAAGCGAAGCGCGA 420
QY 498 GAAAGCAAGCCCG 557
DB 421 GAAAGCAAGCCCG 479
QY 558 GGTGACGAGATCTCGATGAGCTCGTCCGTGCGGAGAGAGCAAGCAAGCGCGGATCAG 617
DB 480 GGTGACGAGATCTCGATGAGCTCGTCCGTGCGGAGAGAGCAAGCAAGCGCGGATCAG 539
QY 618 CTGCGCGTCCGCGCTCGTGTGCGCCAGAGAGAGCTCTTCACTTCGCTTCCAGAG 677
DB 540 CTGCGCGTCCGCGCTCGTGTGCGCCAGAGAGAGAGCTCTTCACTTCGAGAG 599
QY 678 GTTCCAGATCCAGCAGAGCTTCTGCTCGGAGAGCGTGTGATGCGCGTGGAGGGTACGA 737
DB 600 GTTCCAGATCCAGCAGAGCTTCTGCTCGGAGAGCGTGTGATGCGCGTGGAGGGTACGA 659
QY 738 CGTGTCCATGAGAGCCCGGCGAGCGCTTGTGCGCGCGCATCGCGCGAGATGACTA 797
DB 660 CGTGTCCATGAGAGCCCGGCGAGCGCTTGTGCGCGCGCATCGCGCGAGATGACTA 719
QY 798 CTGAGCTCGAGAGTTCATGAGATCCGCGCAAGCGCAAGCTTGGCGGAGATCTAG 852
DB 720 CTGAGCTCGAGAGTTCATGAGATCCGCGCAAGCGCAAGCTTGGCGGAGATCTAG 774
RESULT 5
ACL30325
ID ACL30325 standard; cDNA; 774 BP.
XX
XX ACL30325;
XX
AC ACL30325;
XX
DT 02-JUN-2005 (first entry)
XX
DE Rice abiotic stress responsive polynucleotide SEQ ID NO:8503.
XX
XX ss; abiotic stress tolerance; transgenic plant; plant; cereal;
XX agriculture.
XX
XX Oryza sativa.
XX
XX WO2003008540-A2.
XX
PN WO2003008540-A2.
XX
PD 30-JAN-2003.
XX
PF 21-JUN-2002; 2002WO-US019668.
XX
PR 22-JUN-2001; 2001US-0300112P.
PR 24-AUG-2001; 2001US-0314662P.
PR 26-SEP-2001; 2001US-0325277P.
PR 21-NOV-2001; 2001US-0332132P.
XX
XX (SYGN) SYNGENTA PARTICIPATIONS AG.
XX
PI Krepe J, Briggs SP, Cooper B, Glazebrook J, Goff SA, Katagiri F;
PI Moughamer T, Provart N, Rieke D, Zhu T;
PI MPI: 2003-248011/24.
DR
XX
XX New stress-responsive nucleic acid, useful for altering the
XX responsiveness of a plant, e.g. cereal, to an abiotic stress such as cold
XX stress, salt stress or osmotic stress.
XX
XX Claim 1; SEQ ID NO 8503; 89pp; English.
XX

CC The invention relates to novel abiotic stress responsive polynucleotides
 CC and polypeptides. Also disclosed are vectors, expression cassettes, host
 CC cells, and plants containing such polynucleotides. Also disclosed are
 CC methods for using the polynucleotides and polypeptides to alter the
 CC responsiveness of a plant to abiotic stress. The invention is useful in
 CC agriculture. The nucleic acid is useful for determining whether a test
 CC plant has been exposed to an abiotic stress condition. It is also useful
 CC for selecting an agent that alters abiotic stress regulated.
 CC polynucleotide expression in a plant cell, and to identify a homolog or
 CC ortholog to an abiotic stress responsive polynucleotide. The nucleic acid
 CC molecule and the polypeptide encoded by it are useful in altering the
 CC responsiveness of a plant to an abiotic stress, such as cold stress, salt
 CC stress, osmotic stress or any of their combinations. The present sequence
 CC is used in the exemplification of the invention
 XX

Sequence 774 BP; 150 A; 248 C; 269 G; 107 T; 0 U; 0 Other;

Query Match 61.9%; Score 744.6; DB 11; Length 774;
 Best Local Similarity 99.2%; Pred. No. 1.1e-137;

Matches 769; Conservative 0; Mismatches 4; Indels 2; Gaps 2;

QY 79 ATGGGAGGCTCTCGTCTGCGAAGATGGGCTCAAGAGGCTCATGAGCGCGGAG 138
 DB 1 ATGGGAGGCTCTCGTCTGCGAAGATGGGCTCAAGAGGCTCATGAGCGCGGAG 60
 QY 139 GAGGACAAAGTCTCTCGTCTGCGAAGATGGGCTCAAGAGGCTCATGAGCGCGGAG 198
 DB 61 GAGGACAAAGTCTCTCGTCTGCGAAGATGGGCTCAAGAGGCTCATGAGCGCGGAG 120
 QY 139 CCCAAGCAAGCGGCTGCTGCGTTCGCGCAAGAGTGCCTCGGCTGATCAATCAG 258
 DB 121 CCCAAGCAAGCGGCTGCTGCGTTCGCGCAAGAGTGCCTCGGCTGATCAATCAG 180
 QY 259 CTGGCGCCGACATCAAGCGGCGCACTTCTCCAGAGAGAGGACACCATATCAT 318
 DB 181 CTGGCGCCGACATCAAGCGGCGCACTTCTCCAGAGAGAGGACACCATATCAT 240
 QY 319 CTCCAAGAGCTGTTGGCAACAGTGTCTCCGAATTGCGCGCAAGTTCGCGGAGAGAG 378
 DB 241 CTCCAAGAGCTGTTGGCAACAGTGTCTCCGAATTGCGCGCAAGTTCGCGGAGAGAG 300
 QY 379 GACAAAGAGATCAAGAGCTGTGGACAC-ACCACTCAAGAGCGCTCATGAGCGCGG 437
 DB 301 GACAAAGAGATCAAGAGCTGTGGACACACCACTCAAGAGCGCTCATGAGCGCGG 360
 QY 438 TCAGGCGGCTCATGTTCGCGCGCAAGAGCAAGAGCAAGAGCGCAAGAGCGGAG 497
 DB 361 TCAGGCGGCTCATGTTCGCGCGCAAGAGCGGCAAGAGCAAGAGCGGAGCGGAG 420
 QY 498 GAAAGCAGCG 557
 DB 421 GAAAGCAGCG 479
 QY 558 GGTGACGAGTCTCTGATGAGTCTCTGATGAGTCTCTGATGAGTCTCTGATGAG 617
 DB 480 GGTGACGAGTCTCTGATGAGTCTCTGATGAGTCTCTGATGAGTCTCTGATGAG 539
 QY 618 CTGGCGCTGCGGCTCTGATGAGTCTCTGATGAGTCTCTGATGAGTCTCTGATGAG 677
 DB 540 CTGGCGCTGCGGCTCTGATGAGTCTCTGATGAGTCTCTGATGAGTCTCTGATGAG 599
 QY 678 GTTCCAGATTCGAGCAGAGTCTTGTGTCGAGAGCGCTGTGATGAGTCTTGAAG 737
 DB 600 GTTCCAGATTCGAGCAGAGTCTTGTGTCGAGAGCGCTGTGATGAGTCTTGAAG 659
 QY 738 CGTGTTCATGAGAGCGCGGAGCGGCTCTGTCGCGCGCGCATCGCGAGCATGAGACTA 797
 DB 660 CGTGTTCATGAGAGCGCGGAGCGGCTCTGTCGCGCGCGCATCGCGAGCATGAGACTA 719
 QY 798 CTGGCTCGAGAGTGTTCATGAGTCTCGGCGAAGCGCAAGACTTTCGCGAGATCTAG 852
 DB 720 CTGGCTCGAGAGTGTTCATGAGTCTCGGCGAAGCGCAAGACTTTCGCGAGATCTAG 774

RESULT 6

ADD16949; ID ADD16949 standard; DNA; 454 BP.

AC ADD16949;

DT 15-JUN-2004 (first entry)

DE DNA (SeqID 1017) that confers an altered visual phenotype in plants.

XX de; visual phenotype; plant; architecture; leaf surface; chlorotic;

KM bleaching; etching; wet leaf; stunting; elongation; texture;

KM agronomic trait; growth regulation; dwarf variety; insect resistance;

KM heat stress; transgenic.

XX Unidentified.

OS MO2003020741-A1.

PN 13-MAR-2003.

PD 30-AUG-2002; 2002MO-US027880.

PF 31-AUG-2001; 2001US-0316326P.

PR (DOWC) DOW CHEM CO.

PA (DOWC) DOW AGROSCIENTES LLC.

PI Crossley R, Skokut T, Ruegger M, Larrinua I, Shukla V;

DR MPI; 2003-300858/29.

XX Novel isolated nucleic acid derived from *Nicotiana benthamiana*, *Oryzae*

PT sativa, *Saccharomyces cerevisiae*, and *Papaver rhoeas*, useful for

XX conferring altered visual phenotypes in plants.

PS Claim 1; SEQ ID NO 1017; 517bp; English.

XX This invention relates to the identification and isolation of novel

CC nucleic acid molecules that confer altered visual phenotypes in plants.

CC Specifically, it refers to modifications of plant architecture and/or

CC leaf surface features in plants, such as chlorotic, bleaching, etching,

CC wet leaf, stunting, elongation and texture phenotypes, which are thought

CC will be agronomic traits beneficial to the farmer. As such, these novel

CC phenotypes can affect growth regulation i.e. useful for creating dwarf

CC varieties, exhibit resistance to insects or heat stress, confer changes

CC in pigment content such that plants have enhanced vitamin production or

CC delayed senescence and also for example produce plants that control the

CC production of ethylene. Furthermore, the present invention comprises

CC generating transgenic plants, as well as reproducibly altering the visual

CC phenotype of plant seeds, plant tissues and plant cells containing the

CC polynucleotides described herein. This polynucleotide is a homologue of a

CC DNA sequence that confers an altered visual phenotype when expressed in

CC plants, the method of the invention.

Sequence 454 BP; 111 A; 147 C; 141 G; 55 T; 0 U; 0 Other;

Query Match 34.9%; Score 420; DB 10; Length 454;

Best Local Similarity 98.8%; Pred. No. 1.6e-73;

Matches 423; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CAGCGGCTCTCTTCCAGAGACACACACGCAAGAGAGAGAGAGAGAGAGAGAGAG 60
 DB 27 CAGCGGCTCTCTTCCAGAGACACACACGCAAGAGAGAGAGAGAGAGAGAGAGAG 86
 QY 61 AGGAG 120
 DB 87 AGGAG 146
 QY 121 GGTTCATGAGACCGGAG 180
 DB 147 GGTTCATGAGACCGGAG 206

PR 05-NOV-2001; 2001US-00985678.
 XX
 PA (LIU/) LIU J.
 PA (ZHOU/) ZHOU Y.
 PA (KOVA/) KOVALIC D K.
 PA (SCRE/) SCREEN S E.
 PA (TAB/) TABASKA J E.
 PA (CAO/) CAO Y.
 XX
 PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y,
 XX
 DR WPI; 2004-180133/17.
 XX
 PT New recombinant DNA construct, useful for improving plant tolerance to
 PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
 PT pests, for conferring increased resistance to plant disease, or for
 PT improving yield.
 XX
 PS Claim 1: SEQ ID NO 3220; 15pp; English.
 XX
 CC The invention describes a recombinant DNA construct comprising a
 CC polynucleotide consisting of a sequence encoding an amino acid sequence
 CC available in electronic form from the US patent office at
 CC ftp.segdata.uspto.gov/sequence.html?docid:2004034888. The polynucleotide
 CC of the invention are also useful in physical arrays of molecules and as
 CC plant breeding markers. The recombinant DNA construct is useful for
 CC improving plant tolerance to cold, heat, drought, herbicides, extreme
 CC osmotic conditions, pathogens or pests, for manipulating growth rate in
 CC plant cells by modification of the cell cycle pathway, for conferring
 CC increased resistance to plant disease, for producing galactamannan,
 CC lignin or plant growth regulators, for increasing the rate of homologous
 CC recombination in plants, for improving yield by modification of
 CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
 CC or by providing improved plant growth and development under at least one
 CC stress condition or for modifying seed oil or protein yield and/or
 CC content. This sequence represents a plant full length insert
 CC polynucleotide that can be used in the recombinant DNA construct of the
 CC invention.
 XX
 SQ Sequence 1276 BP; 290 A; 401 C; 392 G; 193 T; 0 U; 0 Other:
 XX
 Query Match 31.2%; Score 375.2; DB 13; Length 1276;
 Best Local Similarity 64.6%; Pred. No. 1.4e-64;
 Matches 711; Conservative 0; Mismatches 308; Indels 81; Gaps 7;
 QY 76 ACAATGGGAGGAGGCTCGTCTGCGAGAAAGTGGGCTCAAGAGGCTCCATGACGCCG 135
 DB 171 AGAATGGGAGAGCTCGTCTGCGAGAAAGTGGGCTCAAGAGGCGCATGACGCCG 230
 QY 136 GAGGAGGAGAAAGTCTCTCGCCCAATCCAGCCGCAAGCGGCAACTGCGCCGCG 195
 DB 221 GAGGAGGAGAAAGTCTCTCGCGCACATCCAGAGCTTGGCGCACAGCAACTGCGCGG 290
 QY 196 CTGCCCAAGCAAGCCGGGCTGCTGCTGCGGCAAGAGTGCAGGCTCGGTGATCAAC 255
 DB 291 CTGCCCAAGCAAGCCGGGCTGCTGCGGCTCGGCAAGAGTGCAGGCTCGGTGATCAAC 350
 QY 256 TACCTGCGGCGGAGCATCAAGCGGGCAACTTCTCAAGAGGAGAGGACACCATCATC 315
 DB 351 TACCTGCGGCGGAGCATCAAGCGGGCAACTTCTCAAGAGGAGAGGACACCATCATC 410
 QY 316 CATCTCCAGAGAGTGTGGCAACAGTGTCCGCAATTGCCGCGAGTTGCCCGGAGG 375
 DB 411 ACCCTTCACAGACAGTGTGGCAACAGTGTCCGCAATTGCCGCGAGTTGCCCGGAGG 470
 QY 376 ACGGCAACAGAGATCAAGAGAGTGTGGCAACAGTGTCCGCAATTGCCGCGAGGCGC- 434
 DB 471 ACGGCAACAGAGATCAAGAGAGTGTGGCAACAGTGTCCGCAATTGCCGCGAGGCGC 530
 QY 435 -----GGCTCAGGCGGCTCATGTTCGCGGCGAGCGCG 465
 DB 531 ACCAAGACAGCTGAGAGAGAGAGCAAGCGGGCGCATGAGTGTGATCGCGCGCAGAG 590

QY 466 GCGAAGAGACAGAAAGCCGAAAGAGCGGAGAAAGCCAGCCGCGCGCGCGCGCGCG 525
 DB 591 CGCAGAGAGGCCAAAGCG 650
 QY 526 CCGGCGTCCGCGCGAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 585
 DB 651 GCGACACCG 710
 QY 586 GTGGCGGAG 645
 DB 711 ACGGAGACAG 767
 QY 646 GAGAGAGAGTCTCTCACTCGGCTCCGAGAGTCCAGATCGAGAGAGTCTCTGTCG 705
 DB 768 AGCTTACCTCTGCTCTGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 827
 QY 706 GAGACGCTGTCATGCGCGCTGAGAGCGGATGACG-----TGTC 744
 DB 828 GAGACGCTGTCATGCGCGCTGAGAGCGGATGACG-----TGTC 887
 QY 745 ATGAGACCGCGAGAGCGGCTTCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 789
 DB 888 GCGCGCTTCCGAGAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 947
 QY 790 ATGGAATGAGTGGTGGAGTGTTCATGAGAGTCCGCGAGAGCG--CAAGACTGCGCGAG 846
 DB 948 TTGGAATGAGTGGTGGAGTGTTCATGAGAGTCCGCGAGAGCGCGCAACATGCGCGAG 1007
 QY 847 ATCTAGAG-----AAAGAGAGAAATTTTACGTTCTTCCGTTAATTGAT---TTGTT 897
 DB 1008 GTTTAAGAGCGGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1067
 QY 898 TTTTCTCTCTGCG 957
 DB 1068 CTTTCTCTCTCTGCG 1127
 QY 958 TGAGCAATCATCAAG 1017
 DB 1128 TAATTATAG 1187
 QY 1018 CAGTACCTTGAATGATTAATTTTCTTTTAACTCTCTCTGTATGTATAGAAAGAG 1077
 DB 1188 CATGCATTGATCATCTATCTCTTTGCTTGTGTATTAAGATGATGATGATGATGAT 1247
 QY 1078 GAGATCAGTATGAAACCT 1097
 DB 1248 GATATCGTATGAAACCT 1267
 XX
 RESULT 9
 AD142105
 ID AD142105 standard; DNA; 1352 BP.
 XX
 AC AD142105;
 XX
 DT 22-APR-2004 (first entry)
 XX
 DE Plant transcription factor polynucleotide #314.
 XX
 KW transgenic; plant; enhanced tolerance to abiotic stress;
 KW glycosphoric tolerance; hormone sensitivity; disease resistance;
 KW sugar sensing; flowering; flower structure; stem bifurcation;
 KW branching pattern; apical dominance; trichome; stem morphology;
 KW root growth; root hair; seed development; cell proliferation;
 KW leaf differentiation; premature senescence; necrosis; plant size;
 KW leaf morphology; seed morphology; seed biochemistry; root anthocyanin;
 KW plant anthocyanin; light response; shade avoidance; bioinformatic;
 KW transcription factor; gene; de.
 XX
 OS Zea mays.
 XX
 PN US2004019927-A1.
 XX

PD 29-JAN-2004.
 XX 25-FEB-2003; 2003US-00374780.
 PF 18-APR-2001; 2001US-00837944.
 XX (SHER/) SHERMAN B K.
 PA (RIEC/) RIECHMAN J L.
 PA (JIANG/) JIANG C.
 PA (HEAR/) HEARD J E.
 PA (HAAK/) HAAKE V.
 PA (GREG/) GRELMAN R A.
 PA (RATC/) RATCLIFFE O.
 PA (ADAM/) ADAM L J.
 PA (REUB/) REUBER T L.
 PA (KEDD/) KEDDIE J.
 PA (BROU/) BROUN P E.
 PA (PIGR/) PILGRIM M L.
 PA (DUBE/) DUBBEL A N.
 PA (PINE/) PINEDA O.
 PA (YUGG/) YU G.
 XX Sheaman BK, Riechman JL, Jiang C, Heard JE, Haake V,
 PI Grelman RA, Ratcliffe O, Adam LJ, Reuber TL, Keddie J, Brown PE,
 PI Pilgrim ML, Dubell AN, Pineda O, Yu G;
 XX WPI; 2004-132245/13.
 DR New transgenic plant comprising a recombinant polynucleotide of any one
 PT of more than 500 nucleotide sequences, useful in bioinformatic search
 PT methods.
 XX
 XX Claim 1; SEQ ID NO 568; 435bp; English.
 XX The invention describes a transgenic plant comprising a recombinant
 CC polynucleotide of any one of more than 500 nucleotide sequences fully
 CC defined in the specification or its complement. The method of the
 CC invention can be used to produce a plant having altered traits such as:
 CC enhanced tolerance to abiotic stress; glyphosphate tolerance; hormone
 CC sensitivity; disease resistance; sugar sensing; early or late flowering;
 CC altered flower structure, change in stem bifurcations, altered branching
 CC pattern, reduced apical dominance, reduced trichome density; lack of
 CC trichomes; reduced ectopic trichome development; altered trichome
 CC development; increase in trichome number; altered stem morphology;
 CC increased root growth; increased root hairs; altered seed development;
 CC altered cell proliferation or cell differentiation; rapid development;
 CC premature senescence; increased necrosis; increase in seedling or plant
 CC size; decreased plant size; leaf morphology; seed morphology; seed
 CC biochemistry; increase in root anthocyanins; increase in plant
 CC anthocyanins; or alteration in light response or shade avoidance. The
 CC transgenic plant, polynucleotides and polypeptides are useful in
 CC bioinformatic search methods. This sequence represents a plant
 CC transcription factor, and an orthologue of Arabidopsis thaliana
 CC transcription factors isolated in the invention, that can be used in the
 CC creation of a transgenic plant with altered traits.
 CC
 XX SQ Sequence 1352 BP; 300 A; 431 C; 414 G; 207 T; 0 U; 0 Other;
 Query Match 31.2%; Score 375.2; DB 12; Length 1352;
 Best Local Similarity 64.6%; Pred. No. 1.4e-64;
 Matches 711; Conservative 0; Mismatches 308; Indels 81; Gaps 7;
 QY 76 ACAATGGGAGGCTCCGCTGCGGAGGAGTGGGGCTCAAGAGGGTCCATGAGACGGC 135
 DB 195 AAGATGGGAGGCTCCGCTGCGGAGGAGTGGGGCTCAAGAGGGGSCCATGAGACGGC 254
 QY 136 GAGGAGGAGGATCTCTGCTGCGCCATCCAGCGCCAGCGCCAGCTGCGCGCC 195
 DB 255 GAGGAGGAGGATCTCTGCTGCGCCATCCAGAGCTTGGGCGACAGCAACTGGCGCGG 314
 QY 196 CTGCCCCAAGCAAGCGGGCTGCTGCTTGGGCGCAGAGCTGCCGGCTCCGGTGAATCAAC 255
 DB 315 CTGCCCCAAGCAAGCGGGCTGCTGCTGCGGCGCAGAGAGCTGCCGGCTCCGGTGAATCAAC 374

QY 256 TACCTGGGCGCGGACATCAAGCGGGGCAACTTCTCCAGAGAGAGAGAGACCATCATC 315
 DB 375 TACCTGGCGCGGACATCAAGCGGGGCAACTTCTCCAGAGAGAGAGAGAGAGCCCATCATC 434
 QY 316 CATCTCCAGAGCTGCTTGGCAACAGTGTGTCGCCAATTCGCCAGGTTGCCGGAGG 375
 DB 435 ACCCTCCAGAGAGCTCGGCAACAGTGTGTCGCCAATTCGCCAGGTTGCCGGAGG 494
 QY 376 ACGGCAACGAGATTAAGAGAGTGTGCAACCCACTTCMAAGAACGGCTCGAATGGCC- 434
 DB 495 ACGGCAACGAGATTAAGAGAGTGTGCAACCCACTTCMAAGAACGGCTCGAATGGCC- 554
 QY 435 -----GGCTCAGGCGGCTCATGCGCGGAGCGGC 465
 DB 555 ACCAAGCAGCTGGAGCAGAGCAGACGAGGGGCGCATGCAAGTGTGAGCGCCCGCAGAGAG 614
 QY 466 GGCAGAGAGCAACAGAGACCGAAGAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 525
 DB 615 CGCAGCAGAGCCCAAGCGCGCGGGTGCAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 674
 QY 526 CCGGCTGCGCGGAGCGGTCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 585
 DB 675 GCCACACACCGCGCGCGGCTGGAACGCTGCGCGGCTGCTGCTGCTGCTGCTGCTGCTG 734
 QY 586 GTGGCGGAGAGCAGCAGGCAACCGCGGATCAAGCTCGCGGCTCGCGCTCGCGGAGAG 645
 DB 735 ACGGAGCAG 791
 QY 646 GAGGAGAGCTCTTCACTCGGCTTCCAGAGAGATTCAGATGACAGCAGCAGCTTGTGCTG 705
 DB 792 AGCTTCACTCGGCTTCCAG 851
 QY 706 GAGAGCTGTGATGATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 744
 DB 852 GAGAGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 911
 QY 745 ATGAGAGCGCGGAG 789
 DB 912 GCGCGGCTTCCAG 971
 QY 790 ATGAGACTAGCTGCTGAGAGTTCATGAGAGTCCGCGAGAGAGAGAGAGAGAGAGAGAG 846
 DB 972 TTGAGACTAGCTGCTGAGAGTTCATGAGAGTCCGCGAGAGAGAGAGAGAGAGAGAGAG 1031
 QY 847 ATCTAGAG-----AAGAGAGAGATTTTACCGTTTCTGCTTAATTGAT---TTGTT 897
 DB 1032 GTTTAGAGGCGCAGCGCGCGCGCGAGAAATTTTCAAGTCCCTGCTAATTTGATTCATGTT 1091
 QY 898 TTTTCTCTCTGCGCGCATCTTGGACCGGAGAGCATAGCTAAGCAGAGAGAGAGAGAG 957
 DB 1092 CTTTCTCTCTCTGCGCGCATCTTGGACCGGAGAGCATAGCTAAGCAGAGAGAGAGAGAG 1151
 QY 958 TGAGGAAATCATCAAG 1017
 DB 1152 TAATTAATAG 1211
 QY 1018 CAGTAGCTTTGATTAATTTTCTTTTAACTCTCTCTGTAATGTAAGAGAGAGAGAG 1077
 DB 1212 CATGCCATGAGATTAATTTCTTTGTTGCTTCTTTGTAATTAAGATCATCATGAGAGAG 1271
 QY 1078 GAGATCAGTATGAGAACT 1097
 DB 1272 GATATCGATGAGAACT 1291
 RESULT 10
 AD002648
 ID AD002648 standard; cDNA; 1352 BP.
 XX
 AC AD002648;
 XX
 DT 01-JUL-2004 (first entry)

XX DE Corn orthologue of Thalecress transcription factor, cDNA #22.
 XX KM Corn; transcription factor; ss; gene; plant; transgenic; abiotic stress;
 XX KM cold tolerance; heat tolerance; drought; osmotic stress;
 XX KM phosphate limitation; potassium limitation; nitrogen limitation;
 XX KM hormone sensitivity; disease resistance; sugar sensing; seed germination;
 XX KM flowering; inflorescence architectural change;
 XX KM meristem cell differentiation; phylloclaxy; apical dominance;
 XX KM trichome development; seed development; premature senescence;
 XX KM delayed senescence; lethality; necrosis; plant size; leaf morphology;
 XX KM seed morphology; secondary metabolism; light response; shade avoidance.
 OS Zea mays.
 XX US2004045049-A1.
 XX PD 04-MAR-2004.
 XX PF 10-APR-2003; 2003US-00412699.
 XX PR 13-SEP-1999; 99US-00394519.
 XX PR 21-JAN-2000; 2000US-00489376.
 XX PR 17-FEB-2000; 2000US-00506720.
 XX PR 22-MAR-2000; 2000US-00532591.
 XX PR 22-MAR-2000; 2000US-00533029.
 XX PR 22-MAR-2000; 2000US-00533030.
 XX PR 22-MAR-2000; 2000US-00533392.
 XX PR 22-MAR-2000; 2000US-00533648.
 XX PR 06-APR-2000; 2000WO-US009448.
 XX PR 16-NOV-2000; 2000US-00713994.
 XX PR 27-MAR-2001; 2001US-00819142.
 XX PR 17-APR-2001; 2001US-00837444.
 XX PR 30-JAN-2002; 2002US-00958131.
 XX PR 14-JUN-2002; 2002US-00171468.
 XX PR 09-AUG-2002; 2002US-00235066.
 XX PR 09-AUG-2002; 2002US-00235067.
 XX PR 09-AUG-2002; 2002US-00235068.
 XX PR 17-DEC-2002; 2002US-04341668.
 XX PR 25-FEB-2003; 2003US-00374780.
 XX (ZHAN/) ZHANG J.
 XX (FROM/) FROMM M E.
 XX (HEAR/) HEARD J E.
 XX (RIEC/) RIECHMANN J L.
 XX (ADAM/) ADAM L J.
 XX (BROU/) BROUN P E.
 XX (PINE/) PINEDA O.
 XX (REUB/) REUBER T L.
 XX (KEDD/) KEDDIE J S.
 XX (YUGG/) YU G.
 XX (UTAN/) UTANG C.
 XX (SAMA/) SAMAH R S.
 XX (PILG/) PILGRIM M L.
 XX (CREE/) CREELMAN R A.
 XX (DUBE/) DUBBEL A N.
 XX (RATC/) RATCLIFFE O.
 XX (KUMI/) KUMIMOTO R.
 XX (SHER/) SHERMAN B K.
 XX Zhang J, Fromm ME, Heard JE, Riechmann JL, Adam LJ, Broun PE,
 XX Pineda O, Reuber TM, Keddie JS, Yu G, Jiang C, Samaha RS;
 XX Pilgrim ML, Creelman RA, Dubbel AN, Ratcliffe O, Kumimoto R;
 XX Sherman BK;
 XX WPI, 2004-225755/21.
 XX DR New transgenic plant, useful in developing phenotypes with altered or
 XX PT improved characteristics or traits.
 XX SS Claim 1; SEQ ID NO 1062; 213pp; English.
 XX CC The invention relates to a transgenic plant comprising a recombinant

CC polynucleotide having a polynucleotide sequence or its complementary
 CC sequence comprising a sequence encoding a polypeptide, that initiates
 CC transcription (i.e. a transcription factor) from Arabidopsis, Soybean,
 CC Rice, Rape or Corn, comprising any of the sequences appearing as AD001568
 CC -AD003527 or AD003530-AD003559. Also included are using a transgenic
 CC plant to grow a progeny plant, an expression cassette (comprising a
 CC constitutive, inducible or tissue-specific promoter and a recombinant
 CC polynucleotide described above), a host cell comprising the expression
 CC cassette, producing a modified plant having a modified trait, identifying
 CC a factor that is modulated by or interacts with a polypeptide encoded by
 CC the polynucleotide sequence and identifying at least one downstream
 CC polynucleotide sequence that is subject to a regulatory effect of any of
 CC the polypeptides encoded by the polynucleotide described above. The
 CC transgenic plant is useful for producing a plant that has an altered
 CC trait e.g. an enhanced tolerance to abiotic stress (increased tolerance
 CC to chilling, germination in cold conditions, freezing tolerance, tolerance
 CC to heat, tolerance to drought, tolerance to osmotic stress, tolerance to
 CC salt, tolerance to phosphate limitation, tolerance to potassium
 CC limitation, decreased sensitivity to nitrogen limitation), altered
 CC hormone sensitivity, reduced sensitivity to abscisic acid, an altered
 CC response to ethylene, disease resistance, altered susceptibility to
 CC Botrytis, altered susceptibility to Fusarium, altered susceptibility to
 CC Erysiphe, altered susceptibility to Pseudomonas syringae, altered
 CC susceptibility to Sclerotinia, altered sugar sensing, improved seed
 CC germination and seedling vigor, early flowering, late flowering, extended
 CC period of flowering, an inflorescence architectural change, a change in
 CC stem bifurcations, a lack of a shoot meristem, reduced meristem cell
 CC differentiation, altered phylloclaxy, altered branching pattern, reduced
 CC apical dominance, reduced trichome density, ectopic trichome development,
 CC altered trichome development, altered stem morphology, increased root
 CC growth, increased root hairs, altered seed development, altered cell
 CC proliferation/cell differentiation, premature senescence, delayed
 CC senescence, lethality, increased necrosis, an increase in seedling or
 CC plant size, decreased plant size, a change in leaf morphology, increased
 CC altered leaf development, increased leaf size and mass, glossy leaves,
 CC leaf cell expansion, change in seed morphology, altered seed coloration,
 CC increased seed size, decreased seed size, altered seed shape, change in
 CC leaf biochemistry, increased leaf wax, an alteration in leaf prenyl lipid
 CC content, increased leaf insoluble sugars, decreased leaf insoluble
 CC sugars, increased leaf anthocyanins, an alteration of leaf fatty acid
 CC content, an alteration of leaf glucosinolate content, change in seed
 CC biochemistry, an increase in seed oil content, decrease in seed oil
 CC content, increase in seed fatty acid content, decrease in seed fatty acid
 CC content, increase in seed protein content, decrease in seed protein
 CC content, alteration in seed prenyl lipid content, increase in seed
 CC sterols, upregulation of genes involved in secondary metabolism, increase
 CC in root anthocyanins, increase in plant anthocyanins, and alteration in
 CC light response or shade avoidance. The present sequence encodes an
 CC orthologue of a thalecress transcription factor isolated from Corn.
 XX SQ Sequence 1352 BP; 300 A; 431 C; 414 G; 207 T; 0 U; 0 Other;
 XX Query Match 31.2%; Score 375.2; DB 12; Length 1352;
 XX Best Local Similarity 64.6%; Pred. No. 1.4e-64;
 XX Matches 711; Conservative 0; Mismatches 308; Indels 81; Gaps 7;
 OY 76 ACAATGGGAGGCGCTCCGTCGCGAAGAGTGGGCTTAAGAAGGTCCATGAGCGCG 135
 DB 195 AGAATGGGAGAGCTCCGTCGCGAAGAGTGGGCTTAAGAAGGCGGCAATGAGCGCG 254
 OY 136 GAGGAGGACAAGGTCTCGTCGCGCAATCCAGCGCACGCGCACTGCGCGCC 195
 DB 255 GAGGAGGACAGATCTCGTCGCGCAATCCAGAGCTTGGCCACAGCAATGCGCGCG 314
 OY 196 CTGCCCAAGCAAGCGGCGCTGCTGCGGTGGCGCAAGAGCTGCGGCTCGGTGATCAAC 255
 DB 315 CTGCCCAAGCAAGCGGCGCTGCTGCGGTGGCGCAAGAGCTGCGGCTCGGTGATCAAC 374
 OY 256 TACCTGGCGCGCGAATCAAGGCGGCAACTTCCAGAGGAGAGAGACACCATCACC 315
 DB 375 TACCTGGCGCGCGAATCAAGGCGGCAACTTCCAGAGGAGAGAGACACCATCACC 434
 OY 316 CATTCACAGAGCTGTCGGCAACAGGTGGTCCGCAATTGCCGCCAGGTTGCCGCGAGG 375


```

Db      187 CAACCTGGGCGGCGCTCCCAAGAGACCGGCTTGCTGCGGTGGGCAAGAGCGCGGCT 246
Qy      243 CCGGTGATCAACTACCTGCGCGCGGACATCAAGCGGGCAACTTCTCCAGAGAGAGA 302
Db      247 CCGGTGATCAACTACCTGCGCGCGGACATCAAGCGGGCAACTTCTCCAGAGAGAGA 306
Qy      303 GGACACCATCATCTCACTGAGAGTGTGGCAAGTGTGTCCGCAATTGCGCGCGAG 362
Db      307 GGAAGCATATCAGCTTCCAGAGAGCTCGGCAACAGGTGTGTCCGCAATTGCGCGAG 366
Qy      363 GTTGGCCGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 422
Db      367 GTTGGCCGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 426
Qy      423 CTTGATGC-----GCCGGCTCAAGGGCGGTGATGTGCGCGGAGAGAGAG 464
Db      427 CTTGATGC-----GCCGGCTCAAGGGCGGTGATGTGCGCGGAGAGAGAGAG 486
Qy      465 CCGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 500
Db      487 CCGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 546
Qy      501 GCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 560
Db      547 GACGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 606
Qy      561 GACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 620
Db      607 GACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 666
Qy      621 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 674
Db      667 GCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 726
Qy      675 GAGAGTTCAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 728
Db      727 GAGAGTTCAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 786
Qy      729 GCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 760
Db      787 CAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 846
Qy      761 -----CGTTCGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 809
Db      847 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 906
Qy      810 GTTCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 866
Db      907 GTTCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 966
Qy      867 TTTTACCGTTTCTTGGTTAAT-TGATTTGTTTTTCTCTCTCTCTCTCTCTCTCTCT 925
Db      967 AATTTTGGCTCTTAATGATTCATGCTTTTCTCTCTCTCTCTCTCTCTCTCTCTCT 1026
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```

RESULT 12

AD142101
ID AD142101 standard; DNM; 1344 BP.

AC AD142101;

DT 22-APR-2004 (first entry)

DE Plant transcription factor polynucleotide #310.

XX transgenic; plant; enhanced tolerance to abiotic stress;

KW glycosylase tolerance; hormone sensitivity; disease resistance;

KW sugar sensing; flowering; flower structure; stem bifurcation;

KW branching pattern; apical dominance; trichome; stem morphology;
KW root growth; root hair; seed development; cell proliferation;
KW cell differentiation; premature senescence; necrosis; plant size;
KW leaf morphology; seed morphology; seed biochemistry; root antheranin;
KW plant antheranin; light response; shade avoidance; bioinformatic;
KW transcription factor; gene; ds.

XX Zea mays.

XX US2004019927-A1.

XX 29-JAN-2004.

PF 25-FEB-2003; 2003US-00374780.

PK 18-APR-2001; 2001US-00837944.

XX (SHER/) SHERMAN B K.

XX (RIEC/) RIECHMANN J L.

XX (JIAN/) JIANG C.

XX (HEAR/) HEARD J E.

XX (HAAR/) HAARE V.

XX (CREE/) CREELMAN R A.

XX (RATC/) RATCLIFFE O.

XX (ADAM/) ADAM L J.

XX (REUB/) REUBER T L.

XX (KEDD/) KEDDIE J.

XX (BROU/) BROUN P E.

XX (PILG/) PILGRIM M L.

XX (DUBE/) DUBELL A N.

XX (PINE/) PINEDA O.

XX (YUGG/) YU G.

XX Sherman BK, Riechmann JL, Jiang C, Heard JE, Haake V,

PI Creelman RA, Ratcliffe O, Adam LJ, Reuber TL, Keddie J, Brown PE;

PI Pilgrim ML, Dubell AN, Pineda O, Yu G;

XX WPI; 2004-132245/13.

XX New transgenic plant comprising a recombinant polynucleotide of any one

PT of more than 500 nucleotide sequences, useful in bioinformatic search

PT methods.

XX Claim 1; SEQ ID NO 564; 435bp; English.

XX The invention describes a transgenic plant comprising a recombinant

CC polynucleotide of any one of more than 500 nucleotide sequences fully

CC defined in the specification or its complement. The method of the

CC invention can be used to produce a plant having altered traits such as:

CC enhanced tolerance to abiotic stress; glycosylase tolerance; hormone

CC sensitivity; disease resistance; sugar sensing; early or late flowering;

CC altered flower structure; change in stem bifurcations; altered branching

CC pattern; reduced apical dominance; reduced trichome density; lack of

CC trichomes; reduced ectopic trichome development; altered trichome

CC development; increase in trichome number; altered stem morphology;

CC increased root growth; increased root hairs; altered seed development;

CC altered cell proliferation or cell differentiation; rapid development;

CC premature senescence; increased necrosis; increase in seedling or plant

CC size; decreased plant size; leaf morphology; seed morphology; seed

CC biochemistry; increase in root antheranin; increase in plant

CC antheranin; or alteration in light response or shade avoidance. The

CC transgenic plant, polynucleotides and polypeptides are useful in

CC bioinformatic search methods. This sequence represents a plant

CC transcription factor, and an orthologue of Arabidopsis thaliana

CC transcription factors isolated in the invention, that can be used in the

CC creation of a transgenic plant with altered traits.

XX Sequence 1344 BP; 306 A; 437 C; 401 G; 200 T; 0 U; 0 Other;

XX Query Match 30.4%; Score 366; DB 12; Length 1344;

XX Best Local Similarity 65.7%; Pred. No. 9, 1e-63;

XX Matches 706; Conservative 0; Mismatches 270; Indels 98; Gaps 8;

XX New transgenic plant, useful in developing phenotypes with altered or
 PT improved characteristic or traits.
 XX

PS Claim 1; SEQ ID NO 1058; 213pp; English.

XX The invention relates to a transgenic plant comprising a recombinant
 CC polynucleotide having a polynucleotide sequence or its complementary
 CC sequence comprising a sequence encoding a polypeptide, that initiates
 CC transcription (i.e. a transcription factor) from Arabidopsis, Soybean,
 CC Rice, Rape or Corn, comprising any of the sequences appearing as AD001588
 CC AD003327 or AD003530-AD003559. Also included are using a transgenic
 CC plant to grow a progeny plant, an expression cassette (comprising a
 CC constitutive, inducible or tissue-specific promoter and a recombinant
 CC polynucleotide described above), a host cell comprising the expression
 CC cassette, producing a modified plant having a modified trait, identifying
 CC a factor that is modulated by or interacts with a polypeptide encoded by
 CC the polynucleotide sequence and identifying at least one downstream
 CC polynucleotide sequence that is subject to a regulatory effect of any of
 CC the polypeptides encoded by the polynucleotide described above. The
 CC transgenic plant is useful for producing a plant that has an altered
 CC trait e.g. an enhanced tolerance to abiotic stress (increased tolerance
 CC to chilling, germination in cold conditions, freezing tolerance, tolerance
 CC to heat, tolerance to drought, tolerance to osmotic stress, tolerance to
 CC salt, tolerance to phosphate limitation, tolerance to potassium
 CC limitation, decreased sensitivity to nitrogen limitation), altered
 CC hormone sensitivity, reduced sensitivity to abscisic acid, an altered
 CC response to ethylene, disease resistance, altered susceptibility to
 CC Botrytis, altered susceptibility to Fusarium, altered susceptibility to
 CC Sclerotinia, altered susceptibility to Pseudomonas syringae, altered
 CC susceptibility to Scierotinia, altered sugar sensing, improved seed
 CC germination and seedling vigor, early flowering, late flowering, extended
 CC period of flowering, an inflorescence architectural change, a change in
 CC stem bifurcation, a lack of a shoot meristem, reduced meristem cell
 CC differentiation, altered phyllotaxy, altered branching pattern, reduced
 CC apical dominance, reduced trichome density, ectopic trichome development,
 CC altered trichome development, altered stem morphology, increased root
 CC growth, increased root hairs, altered seed development, altered cell
 CC proliferation/cell differentiation, premature senescence, delayed
 CC senescence, lethality, increased necrosis, an increase in seedling or
 CC plant size, decreased plant size, a change in leaf morphology, increased
 CC altered leaf development, increased leaf size and mass, glossy leaves,
 CC leaf cell expansion, change in seed morphology, altered seed coloration,
 CC increased seed size, decreased seed size, altered seed shape, change in
 CC leaf biochemistry, increased leaf wax, an alteration in leaf prenyl lipid
 CC content, increased leaf inosoluble sugars, decreased leaf insoluble
 CC sugars, increased leaf anthocyanins, an alteration of leaf fatty acid
 CC content, an alteration of leaf glucosinolate content, change in seed
 CC biochemistry, an increase in seed oil content, decrease in seed oil
 CC content, increase in seed fatty acid content, decrease in seed fatty acid
 CC content, increase in seed protein content, decrease in seed protein
 CC content, alteration in seed prenyl lipid content, increase in seed
 CC sterols, upregulation of genes involved in secondary metabolism, increase
 CC in root anthocyanins, increase in plant anthocyanins, and alteration in
 CC light response or shade avoidance. The present sequence encodes an
 CC orthologue of a chalcress transcription factor isolated from Corn.
 XX

Sequence 1344 BP; 306 A; 437 C; 401 G; 200 T; 0 U; 0 Other;

Query Match 30.4%; Score 366; DB 12; Length 1344;
 Best Local Similarity 65.7%; Pred. No. 9; 1e-63;
 Matches 706; Conservative 0; Mismatches 270; Indels 98; Gaps 8;

QY 3 GCCGCTCTCTTCCAAACACACACGAGAGAGACGACGACTTACATCAGAGCAG 62
 DB 43 GCTCCCTCCCTCCGCCCCAACAGCA-AAACAGGCGAGCAGCAACACACGCTCGAACCGG 101
 QY 63 GGAAGGACGACGACAAATGGGGAGGCTCCGTCGCGAGAGATGGGGCTCAAGAGG 122
 DB 102 ACAAGCCATCCCAATATATGGGAGGCTCCGTCGCGAGAGATGGGGCTCAAGAGG 161
 QY 123 TCCATGACGCGGAGAGAGACAGGTCTCTGTCGCCCATTCAGCGGCACGGCAGCG 182

DB 162 GGCATGAGACCCCGAGAGAGACAAAGGTCTCGGTGCGCCACATCCAGAGCTTGCCGACAG 221
 QY 183 CAATGCGCGCCCTTGCCCAAGCAGCCGGGCTGCTGCGTTGGCGCAAGAGCTGCCGCT 242
 DB 222 CAATGCGCGCGCTGCCCCAGCAGCCGCTTGCTGCGGTGGGCAAGAGCTGCCGCT 281
 QY 243 CCGGTGATCACTACCTGCGCGCCGAGCATCAAGCGGGGCACTTCCAGAGAGAGG 302
 DB 282 CCGGTGATCACTACCTGCGCGCCGAGCATCAAGCGGGGCACTTCCAGAGAGAGG 341
 QY 303 GGAACCATCATCATCTCTCAGAGCTGCTGGCAACAGGTGGTCCGCAATTGCCCGCAG 362
 DB 342 GGAACCATCATCATCTCTCAGAGCTGCTGGCAACAGGTGGTCCGCAATTGCCCGCAG 401
 QY 363 GTTGCCCGGAGAGCGGACAGAGATCAAGAACTGTGGCACCCCACTCAAGAGG 422
 DB 402 GCTGCGCGCGCGAGAGACAGAGATCAAGAACTGTGGCACCCCACTCAAGAGG 461
 QY 423 CCGTCAATG-----GCGGCTCAGGCGGATGATGTGCGCGAGCGG 464
 DB 462 CCGTCAATG-----GCGGCTCAGGCGGATGATGTGCGCGAGCGG 521
 QY 465 CCGCAAGAGACAGAGAGAGCGAGAGAGCG-----GAAGAA 500
 DB 522 CCGCAAGAGACAGAGAGAGCGAGAGAGCG-----GAAGAA 581
 QY 501 GCGAGCG 560
 DB 582 GAGCG 641
 QY 561 GACGAGCTGCTGATGAGCGCTGCGCGCGCGAGAGAGAGCGCGCGCGCGCGCGCGCG 620
 DB 642 GCGCTGCTGCTGATGAGCGCTGCGCGCGAGAGAGAGCGCGCGCGCGCGCGCGCGCG 701
 QY 621 GCGCTGCG 674
 DB 702 GCGGAGCTGCG 761
 QY 675 GGAATTCAGATGACAGAGAGCTTTGTGCGAGAGCGTGTGATGCCCTGGA----- 728
 DB 762 GAGATTCAGATGACAGAGAGCTTTGTGCGAGAGCGTGTGATGCCCTGGA----- 821
 QY 729 CGGATACAGCGTGCATGAGAGCGCGCGAGCG----- 760
 DB 822 CGAGAGCTGCTGCG 881
 QY 761 -----CGTTGCTGCG 809
 DB 882 GCGCGCGCGCGCTCTCTGCTGCGTGGGCGCGAGCGCGCGCGCGCGCGCGCGCGCGCG 941
 QY 810 GTTCATGAGTCCGCGGAAAGCGCA---AGACTTCCCGAGATCTAGAGAAAGAGAGAA 866
 DB 942 GTTCATGAGTCCGCGGAAAGCGCA---AGACTTCCCGAGATCTAGAGAAAGAGAGAA 1001
 QY 867 TTTTCCGTTTGGTTAT-TGATTTGTTTTCCTCTGCGCGCATCTTGCACG 925
 DB 1002 AATTTTGGCTCTTAATGATTCATGTTCTTTCTCTCTCTCTCTCTCTCTCTCTCTCT 1061
 QY 926 GAGAGACATGACTAACAAGAGAGAGTGTCTAGAGCAATCATCAAGAGAGAA 979
 DB 1062 CTTCATGAG 1115

RESULT 14

ADXS0163
 ID ADXS0163 standard; cDNA; 1126 BP.

XX ADXS0163;

XX 21-APR-2005 (first entry)

XX Plant full length insert polynucleotide seqid 24903.

KM plant protectant; plant growth regulant; gene therapy; plant;
 KM recombinant DNA construct; physical array; plant breeding marker;
 KM cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
 KM extreme osmotic condition; pathogen tolerance; pest tolerance;
 KM galactomannan production; lignin production; disease resistance;
 KM yield; plant growth; plant development; seed oil; protein yield;
 KM protein content; gene; ss.
 XX unidentified.
 OS
 XX US2004034888-A1.
 PN
 XX 19-FEB-2004.
 PD
 XX 28-APR-2003; 2003US-00425114.
 PF
 XX 06-MAY-1999; 99US-00304517.
 PR 05-NOV-2001; 2001US-00985678.
 XX
 XX (LIUJ/), LIU J.
 PA (ZHOU/), ZHOU Y.
 PA (KOVA/), KOVALIC D K.
 PA (SCRE/), SCREEN S E.
 PA (TABAS/), TABASKA J E.
 PA (CAOY/), CAO Y.
 XX
 PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
 DR WPI, 2004-180133/17.
 XX
 PT New recombinant DNA construct, useful for improving plant tolerance to
 PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
 PT pests, for conferring increased resistance to plant disease, or for
 PT improving yield.
 XX
 PS Claim 1; SEQ ID NO 24903; 15bp; English.
 XX
 CC The invention describes a recombinant DNA construct comprising a
 CC polynucleotide consisting of a sequence encoding an amino acid sequence
 CC available in electronic form from the US patent office at
 CC ftp://seedate.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide
 CC of the invention are also useful in physical arrays of molecules and as
 CC plant breeding markers. The recombinant DNA construct is useful for
 CC improving plant tolerance to cold, heat, drought, herbicides, extreme
 CC osmotic conditions, pathogens or pests, for manipulating growth rate in
 CC plant cells by modification of the cell cycle pathway, for conferring
 CC increased resistance to plant disease, for producing galactomannan,
 CC lignin or plant growth regulators, for increasing the rate of homologous
 CC recombination in plants, for improving yield by modification of
 CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
 CC or by providing improved plant growth and development under at least one
 CC stress condition or for modifying seed oil or protein yield and/or
 CC content. This sequence represents a plant full length insert
 CC polynucleotide that can be used in the recombinant DNA construct of the
 CC invention.
 CC
 XX
 XX Sequence 1126 BP; 239 A; 378 C; 360 G; 149 T; 0 U; 0 Other;
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 Query Match 29.3%; Score 352.6; DB 13; Length 1126;
 Best Local Similarity 66.8%; Pred. No. 4e-60;
 Matches 683; Conservative 0; Mismatches 224; Indels 116; Gaps 8;

DB 194 CTGCCAAGCAAGCGGCTGCTGCGGCGCAAGAGCTGCCGCTCCGGTGAATCAAC 253
 QY 256 TACCTCGCGCGGACATTAACGGGGCACTTTCTCAGAGAGAGAGACACCTATC 315
 DB 254 TACCTCGCGCGGACATTAACGGGGCACTTTCTCAGAGAGAGAGACACCTATC 313
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 DB 314 AGCTTCCAGAGCACTCGGCAACAGGTGTCGCCAATTGCGCGCAGGTGCGCGGAGG 373
 QY 376 ACGAACAAGATCAAGACGTGTGCAACCCACTCAAGAAAGCGCTCGATC---- 431
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 DB 434 AAGCAGAGCAGCAGCAGCAACAGCGGAGCAAGCGCGGCTGCGCGGCAAGAGCA 493
 QY 478 AAGAAAGCGAAGAGCGCAAG-----AAGCA 504
 DB 494 AGGCGCGCAGCGCGCGCAAGCGCGGGCGCGGAGCGAAGAGCGACCGCAACGCG 553
 QY 505 GCCCG 555
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 QY 556 TCGGAGAGAGTCTTCATGAGCTTCCTGCGGAGAGAGAGAGAGAGAGAGAGAGAG 615
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 QY 616 AGCTCG 669
 DB 674 AAGCAG 733
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 DB 734 GCCGAGAGAGTTCAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 793
 QY 729 -----CGGTAAGAGTTCATGAGAGCGCGCGAG----- 760
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 QY 761 -----CGTTCG 807
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 QY 808 GTGCTTCAGAGAGTTCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 864
 DB 914 GTGCTTCAGAGAGTTCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 973
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 DB 974 AGAATTTTCGGCTCTTAATTGATTAATGATTAATGATTAATGATTAATGATTAAT 1033
 QY 920 TGCACCGAGAGAGATTAAGTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 979
 DB 1034 TGCATCGAG 1093
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 RESULT 15
 ADI42104 standard; DNA, 1492 BP.
 ID ADI42104
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 AC ADI42104;
 XX
 DT 22-APR-2004 (first entry)
 XX
 DE Plant transcription factor polynucleotide #313.
 XX

Db 1139 GAA 1141

Search completed: June 24, 2006, 19:33:39
Job time : 1462 secs

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: June 25, 2006, 07:42:57 ; Search time 6808 Seconds
(without alignments) 11290.364 Million cell updates/sec

Title: US-10-521-811-1

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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8: gb_sy:*
9: gb_un:*
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14: gb_cm:*
15: gb_da:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1202	100.0	1202	4	OSMYB1202
2	1192.8	99.2	1207	4	AY323484 Oryza sat
3	849	70.6	110000	4	AP008210_258
4	849	70.6	139080	4	OSJN00262
5	846	70.4	1836	4	AK111798 Oryza sat
6	752.6	62.6	816	2	AK659818 Sequence
7	744.6	61.9	774	2	AK653407 Sequence
8	744.6	61.9	774	2	AK660354 Sequence
9	546.4	45.5	673	4	AF467733 Oryza sat
10	436.8	36.3	1044	4	AY615199 Triticum
11	380.8	31.7	1180	4	HVMYB4TRF
12	326.6	27.2	1038	4	AK112056 Oryza sat
13	284.2	23.6	672	2	AK653760 Sequence
14	269.2	22.4	330	4	AY178579
15	269.2	22.4	1084	4	OSMYB1084
16	269.2	22.4	1326	4	AK109011 Oryza sat
17	268.8	22.4	834	2	AK652852 Sequence
18	251.8	20.9	1399	4	AK108621 Oryza sat

19	249	20.7	1637	4	AK11960
20	248.2	20.6	1163	4	AK107483
21	245.8	20.4	1023	2	AX652823
22	245.8	20.4	1528	4	AK111933
23	244.2	20.3	1665	4	AK111720
24	241.2	20.1	966	2	CS137754
25	234.8	19.5	1355	4	OSMYB1355
26	234	19.5	1107	2	AK653762
27	223	19.4	1223	4	AY323480
28	231.4	19.3	1026	2	CS137758
29	228.2	19.0	1336	4	BT009312
30	227.6	18.9	1027	2	CS138020
31	227.6	18.9	1027	4	AK063027
32	225.8	18.8	1069	2	CS137822
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35	223.6	18.6	1450	4	AK111740
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45	217.8	18.1	1389	4	AK064679

ALIGNMENTS

RESULT 1
LOCUS OSMYB1202
DEFINITION O.sativa mRNA for myb factor, 1202 bp.
ACCESSION Y11414
VERSION Y11414.1 GI:1946264
KEYWORDS myb gene.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BBP clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 Pandolfi,D., Solinas,G., Valle,G. and Coraggio,I.
AUTHORS The electronic Plant Gene Register
TITLE Plant Physiol. 114 (2), 747-749 (1997)
JOURNAL 9235602
PUBMED 2 (bases 1 to 1202)
AUTHORS Coraggio,I.
TITLE Direct Submission
JOURNAL Submitted (21-FEB-1997) I. Coraggio, Istituto Biosintesi Vegetali, CNR, Via Bassini 15,, 20133, Milano, ITALY
FEATURES
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REFERENCE
1 Feng, Q., Zhang, Y., Hao, P., Wang, S., Fu, G., Huang, Y., Li, Y., Zhu, J.,
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JOURNAL Lu, X., Li, C., Mu, Y., Sun, T., Lei, H., Li, T., Hu, H., Guan, J.,
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Zhang, Y., Chen, J., Kang, H., Chen, X., Shao, C., Sun, Y., Hu, Q.,
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N. L., Zhu, F., Chen, W., Lan, L., Lai, Y., Cheng, Z., Gu, M., Jiang, J.,
Li, J., Hong, G., Xue, Y. and Han, B.
Sequence and analysis of rice chromosome 4
Nucleic Acids Res 34(13): 316-320 (2006)
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Han, B., Feng, Q., Huang, Y., C., Li, Y., Zhu, J., Zhao, Q., Hu, X.,
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Ding, C., W., Sheng, H., H., Gu, J., L., Chen, S., T., N. L., Zhu, F., H. and
Hong, G., F.
Direct Submission
Submitted (04-MAY-2002) Han Bin, National Center for Gene Research,
Chinese Academy of Sciences, 500# Cao Bao Road, Shanghai 200233,
CHINA. E-mail enquiries: bhan@ncgr.ac.cn. Clone requests:
bhan@ncgr.ac.cn
Oryza sativa japonica (nipponbare) genomic DNA, chromosome 4, BAC
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On Jan 14, 2005 this sequence version replaced gi:38568055.
Web site: http://www.ncgr.ac.cn
----- Summary Statistics -----
Assembly program: phrap
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This is a complete sequence.
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 Db 33891 GCACGCTAA 33883
 RESULT 5
 AK11798
 LOCUS AK11798
 DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone:023105H16, full insert sequence.
 ACCESSION AK11798
 VERSION AK11798.1 GI:37988461
 KEYWORDS FLI CDNA; CAP trapper.
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Bep Clade; Ehrhartoideae; Oryzeae; Oryza.
 REFERENCE
 AUTHORS
 1
 The Rice Full-length cDNA Consortium, National Institute of Agrobiological Sciences Rice Full-length cDNA Project Team; Kikuchi, S., Satoh, K., Negata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yasaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuka, K., Shishiki, T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group; Ootomo, Y., Murakami, K., Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y., Kurosaki, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, Q., Lu, M., Narikawa, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Nikiura, J., Ikeda, R., Ishibiki, J., Kawamata, M., Yoshimura, A., Miura, J., Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Matsubara, K., RIKEN, Kawai, J., Carninci, P., Adachi, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hasehida, W., Hayatsu, N., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kondo, S., Kono, H., Miyazaki, A., Osato, N., Ota, Y., Saito, R., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Yoshino, M., and Hayashizaki, Y.
 TITLE
 Collection, mapping, and annotation of over 28,000 cDNA clones from japonica rice
 JOURNAL
 PUBMED
 12869764
 REFERENCE
 AUTHORS
 2
 Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K., Fujimura, T., Fukuda, S., Haneagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayashizaki, Y., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Hotta, I., Iida, J., Iida, Y., Ikeda, R., Imamura, K.,

Imotani, K., Ishibiki, J., Ishii, Y., Ishikawa, M., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawagashira, N., Kawai, J., Kawamata, M., Kikuchi, S., Kishikawa-Hirozane, T., Kishimoto, N., Kobayashi, M., Kodama, T., Kojima, K., Kojima, Y., Kondo, S., Kono, H., Kouda, M., Koya, S., Kuribara, C., Kurosaki, T., Kusumegi, T., Li, C., Lu, M., Masuda, H., Matsubara, K., Matsuyama, T., Miura, J., Miyazaki, A., Mizuno, K., Murakami, K., Murata, M., Negata, T., Nakahama, Y., Nakamura, M., Namiki, T., Narikawa, R., Nikiura, J., Nishi, K., Nomura, K., Nunasaki, R., Ohneda, E., Ohno, M., Ohtsuka, K., Oka, M., Ooka, H., Osato, N., Ota, Y., Ootomo, Y., Ryu, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Satoh, K., Shibata, K., Shinagawa, A., Shiraki, T., Shishiki, T., Sogabe, Y., Sugano, S., Sugiyama, A., Suzuki, K., Suzuki, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Tsunoda, Y., Ueda, M., Waki, K., Xie, Q., Yahagi, W., Yamada, H., Yamamoto, M., Yasunishi, A., Yasaki, J., Yokomizo, S., and Yoshimura, A.
 Rice full-length cDNA
 3 (bases 1 to 1836)
 TITLE
 JOURNAL
 REFERENCE
 AUTHORS
 Kikuchi, S.
 DIRECT Submission
 Submitted (12-SEP-2002) Shoshi Kikuchi, National Institute of Agrobiological Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan (E-mail:ekikuchi@ias.affrc.go.jp, Tel:81-29-838-7007, Fax:81-29-838-7007)
 This clone is one of the 32k full-length cDNA clones from japonica rice.
 URL: http://cdna01.dna.affrc.go.jp/cDNA/
 NIAS Rice Full-length cDNA Project Team: Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yasaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuka, K., Shishiki, T., Yamamoto, M., and Nakahama, Y.
 FAIS Genome Sequencing & Analysis Group: Ootomo, Y., Iida, Y., Fujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Narikawa, R., Kodama, T., Kurosaki, T., Kusumegi, T., Lu, M., Masuda, H., Miura, J., Mizuno, K., Narikawa, R., Nikiura, J., Oka, M., Ryu, R., Sugano, S., Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S., Yoshimura, A., Matsubara, K., and Murakami, K.
 Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Haneagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Iida, J., Imamura, K., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawai, J., Kishikawa-Hirozane, T., Kojima, Y., Kondo, S., Kono, H., Kouda, M., Koya, S., Kuribara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Nunasaki, R., Ohno, M., Osato, N., Ota, Y., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Waki, K., Yasunishi, A., and Hayashizaki, Y.
 Location/Qualifiers
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 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nipponbare"
 /db_xref="taxon:39947"
 /clone="U023105H16"
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 Query Match 70.4%; Score 846; DB 4; Length 1836;
 Best Local Similarity 100.0%; Pred. No. 6.7e-20;
 Matches 846; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 339 CAGGTGTCGCGCAATTTGCCGCGAGTGGCCGAGAGAGCGCAACGAGATCAAGAACT 398
 Db 991 CAGGTGTCGCGCAATTTGCCGCGAGTGGCCGAGAGAGCGCAACGAGATCAAGAACT 1050

Oy	399	TTGGCACAACCACTTCAAGAAAGCGGCTGATACCGCGGCTCAAGGGCGGTTCAATGTGCGGGC	458
Db	1051	GTGGCACAACCACTTCAAGAAAGCGGCTGATGCGCGGCTCAAGGGCGGTTCAATGTGCGGGC	1110
Oy	459	GAGCGCGCGGCAAGAAACAAGAAAGCCGAAGAGCCGAAGAAAGCAGCGCGCGCGCGC	518
Db	1111	GAGCGCGCGGCAAGAAAGCAAGAAAGCCGAAGAGCCGAAGAAAGCAGCGCGCGCGCGCGC	1170
Oy	519	CGCGCGCGCGGCTGCGCCCGAGCGGTCGCGCTCTGTCGTGCGTGAACGGAAGTCTTGATAGGC	578
Db	1171	CGCGCGCGCGGCTGCGCCCGAGCGGTCGCGCTCTGTCGTGCGTGAACGGAAGTCTTGATAGGC	1230
Oy	579	CTCGTCGCTGGCGGAGAGACAAGGAAAGCGCGGGATTCAGACTCGAGCGTCCGCGTCGATGTG	638
Db	1231	CTCGTCGCTGGCGGAGAGACAAGGAAAGCGCGGGATTCAGACTCGAGCGTCCGCGTCGATGTG	1290
Oy	639	CGCCAAAGAGAGAGACTCTCTTCACTCGGCTTCGAGAGATTCCAGATCGACAGACTT	698
Db	1291	CGCCAAAGAGAGAGACTCTCTTCACTCGGCTTCGAGAGATTCCAGATCGACAGAGCTT	1350
Oy	699	CTGGTCGGAAGACGCTGTGATGTCGCGCTGGAAGCGGATACGACGCTGCATGGAAGCCGGGCA	758
Db	1351	CTGGTCGGAAGACGCTGTGATGTCGCGCTGGAAGCGGATACGACGCTGCATGGAAGCCGGGCA	1410
Oy	759	CGCGTTGCTGCGCGCCGCAATCGCGGACGACATGGAATGAGCTCGAGAGTGTTCATGGA	818
Db	1411	CGCGTTGCTGCGCGCCGCAATCGCGGACGACATGGAATGAGAGTGTTCATGGA	1470
Oy	819	GTCCCGGCGAAGCGGCAAGACTTGGCGGACATCTAGAGAAAGAGAGAAATTTAACGCTTC	878
Db	1471	GTCCCGGCGAAGCGGCAAGACTTGGCGGACATCTAGAGAAAGAGAGAAATTTAACGCTTTC	1530
Oy	879	TTCCGTTAATGATTGTTTTGTTTTTCTCTCTGCGCGCAATCTTGCACCGAGGAGCATAGC	938
Db	1531	TTCCGTTAATGATTGTTTTGTTTTTCTCTCTGCGCGCAATCTTGCACCGAGGAGCATAGC	1590
Oy	939	TAAACGACAAGAGTGTCCATGAGCGAATCATTAACAGAGAAAGCGCAATCATGCGATG	998
Db	1591	TAAACGACAAGAGTGTCCATGAGCGAATCATTAACAGAGAAAGCGCAATCATGCGATG	1650
Oy	999	CGATCGAGTGAATGACACCGAGTAGCTTTGATAGTAAATTTCTTTTCTTTTACCTCTTCC	1058
Db	1651	CGATCGAGTGAATGACACCGAGTAGCTTTGATAGTAAATTTCTTTTCTTTTACCTCTTCC	1710
Oy	1059	TGTATGTATAGAAACAGAAAGAGATCAGTGATCGAAACCTGAGATCCTTCTCAACATGTG	1118
Db	1711	TGTATGTATAGAAACAGAAAGAGATCAGTGATCGAAACCTGAGATCCTTCTCAACATGTG	1770
Oy	1119	CAAAATGGAATCATCAGAAACGGGGCTGCGCGTTCTCATTTGATTAATTAATTAACACTT	1178
Db	1771	CAAAATGGAATCATCAGAAACGGGGCTGCGCGTTCTCATTTGATTAATTAATTAACACTT	1830
Oy	1179	GCACGC 1184	
Db	1831	GCACGC 1836	
RESULT 6			
LOCUS	AX659818	816 bp	DNA
DEFINITION	Sequence 175 from Patent WO03000906.	linear	PAT 22-MAR-2003
ACCESSION	AX659818		
VERSION	AX659818.1	GI:29161908	
KEYWORDS			
SOURCE			
ORGANISM	Oryza sativa		
	Oryza sativa		
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BBP		
	clade; Ehrhartoideae; Oryzaceae; Oryza.		
REFERENCE	1		
AUTHORS	Glazebrook, J., Briggs, S., Cooper, B., Goff, S. A., Moughamer, T.,		
	Kateghiri, F., Kreps, U., Provart, N., Rieke, D. and Zhu, T.		
TITLE	Plant disease resistance genes		

Query Match	62.6%	Score 752.6	DB 2	Length 816
Best Local Similarity	96.4%	Prod. No. 1.8e-117		
Matches 804	Conservative 0	Mismatches 4	Indels 9	Gaps 4
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ORIGIN				
Query Match	62.6%	Score 752.6	DB 2	Length 816
Best Local Similarity	96.4%	Prod. No. 1.8e-117		
Matches 804	Conservative 0	Mismatches 4	Indels 9	Gaps 4
FEATURES	source	1. 816		
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		/mol_type="unassigned DNA"		
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ORIGIN				

DEFINITION	Sequence 3277 from Patent WO03000898.
ACCESSION	AX653407
VERSION	AX653407.1 GI:29156221
KEYWORDS	
SOURCE	
ORGANISM	<i>Oryza sativa</i>
REFERENCE	<i>Oryza sativa</i>
AUTHORS	Chang, H.S., Chen, W., Cooper, B., Glazebrook, J., Goff, S.A., Hou, Y.M., Katagiri, F., Quan, S., Tao, Y., Whitlan, S., Xie, Z., Zhu, T. and Zou, G.
TITLE	Plant genes involved in defense against pathogens
JOURNAL	Patent: WO 03000898-A 3277 03-JAN-2003;
FEATURES	Syngenta Participations AG (CH)
SOURCE	Location/Qualifiers
ORIGIN	1..774
	/organism="Oryza sativa"
	/mol_type="unassigned DNA"
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Query Match	61.9%; Score 744.6; DB 2; Length 774;
Best Local Similarity	99.2%; Pred. No. 1.8e-175;
Matches 769; Conservative	0; Mismatches 4; Indels 2; Gaps 2;
Oy	79 ATGGGAGAGGCTCCGTGTCGAGAAATGGGGCTCAAGAAAGGTCATGACGCCGGAG 138
Db	1 ATGGGAAAGGCTCCGTGTCGAGAAATGGGGCTCAAGAAAGGTCATGACGCCGGAG 60
Oy	139 GAGGCAAGGTCCTGTGCGCCCATCCAGCGCCACGGCCACGGCACTGGCGCGCCTG 198
Db	61 GAGGCAAGGTCCTGTGCGCCCATCCAGCGCCACGGCCACGGCACTGGCGCGCCTG 120
Oy	199 CCCAAGCAAGCCGGGCTGCTGCTGTGGCGCAAGAGCTGCGGCTCCGTGATCAACTAC 258
Db	121 CCCAAGCAAGCCGGGCTGCTGCTGTGGCGCAAGAGCTGCGGCTCCGTGATCAACTAC 180
Oy	259 CTGGCGGCGGACATCAAGCGGGGGCAACTTCTCAAGAGAGAGAGAGACCATCATTCAT 318
Db	181 CTGGCGGCGGACATCAAGCGGGGGCAACTTCTCAAGAGAGAGAGAGACCATCATTCAT 240
Oy	319 CTCCACGAGCTGCTTGGCAACAGGTGTCGCAATTGCGCGCAGGTTGCCCGGAGACG 378
Db	241 CTCCACGAGCTGCTTGGCAACAGGTGTCGCAATTGCGCGCAGGTTGCCCGGAGACG 300
Oy	379 GACAAAGAGATCAAGACGTTGTGGAC- ACCCACTTCAAGAACGGCTTCGATGCGCGGC 437
Db	301 GACAAAGAGATCAAGACGTTGTGGAC- ACCCACTTCAAGAACGGCTTCGATGCGCGGC 360
Oy	438 TCAGGCGGTCATGTGTCGGGAGGCGGGGCGAAGAGCAAGAACCGGAAGAGCGCGAA 497
Db	361 TCAGGCGGTCATGTGTCGGGAGGCGGGGCGAAGAGCAAGAACCGGAAGAGCGCGAA 420
Oy	498 GAAAGCAAGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTCGTCGTC 557
Db	421 GAAAGCAAGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTCGTCGTC 479
Oy	558 GGTGACGAGTCTTGATGGCTCGTGGGTGGCGGAGGACGCGCAACGCCGGAGTACG 617
Db	480 GGTGACGAGTCTTGATGGCTCGTGGGTGGCGGAGGACGCGCAACGCCGGAGTACG 539
Oy	618 CTCGGCGTCGCGTCGCGTCGCGTCGCGTCGCGTCGCGTCGCGTCGCGTCGCGTCGCG 677
Db	540 CTCGGCGTCGCGTCGCGTCGCGTCGCGTCGCGTCGCGTCGCGTCGCGTCGCGTCGCG 599
Oy	678 GTTCAGATCGACGACAGCTTGTGTCGAGAGCGCTGTGATGCGCGTCGAGCGAGTACA 737
Db	600 GTTCAGATCGACGACAGCTTGTGTCGAGAGCGCTGTGATGCGCGTCGAGCGAGTACA 659
Oy	738 CGTGTCAATGAGCCCGGCGACGCGTTCGTGTCGCGCGCCATTCGCGCAAGCATGACTTA 797
Db	660 CGTGTCAATGAGCCCGGCGACGCGTTCGTGTCGCGCGCCATTCGCGCAAGCATGACTTA 719

Oy	798	CTGGCTCGAGATGTTTCAATGAGAGTCGGCGGAACGCCAAGACTTGCCCGCAGATCTTG	852
Db	720	CTGGCTCGAGATGTTTCAATGAGAGTCGGCGGAACGCCAAGACTTGCCCGCAGATCTTG	774
RESULT 8			
AX660364			
LOCUS	AX660364	774 bp	DNA linear PAT 22-MAR-2003
DEFINITION	Sequence 721 from Patent WO03000906.		
ACCESSION	AX660364		
VERSION	AX660364.1 GI:29162181		
KEYWORDS			
SOURCE			
ORGANISM	Oryza sativa		
	Euryza sativa		
	Buxatryl, A. Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
	Spermatophytes; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP		
	clade; Ehrhartioideae; Oryzeae; Oryza.		
REFERENCE	1 Glazebrook, J., Briggs, S., Cooper, B., Goff, S.A., Moughamer, T.,		
AUTHORS	Kataagiri, F., Kleps, J., Provart, N., Rieke, D. and Zhu, T.		
TITLE	Plant disease resistance genes		
JOURNAL	Patent: WO 03000906-A 721 03-JAN-2003;		
FEATURES	Syngeta Participations AG (CH)		
source	location/Qualifiers		
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ORIGIN			
Query Match	61.9%; Score 744.6; DB 2; Length 774;		
Best Local Similarity	99.2%; Pred. No. 1.8e-175;		
Matches	769; Conservative 0; Mismatches 4; Indels 2; Gaps 2;		
Oy	79	ATGGGGAAGGCTCCGTCTCGAGAATAAGGAGCTCAAGAAGGCTCCATGAGCCGCGAG	138
Db	1	ATGGGGAAGGCTCCGTCTCGAGAATAAGGAGCTCAAGAAGGCTCCATGAGCCGCGAG	60
Oy	139	GAGACAAGAGTCTCTGTGCCCCACATCCAGCCCAAGCCCAAGCCCAAGCCGCTG	198
Db	61	GAGACAAGAGTCTCTGTGCCCCACATCCAGCCCAAGCCCAAGCCCAAGCCGCTG	120
Oy	199	CCCAAGAACGCGGGGCTGCAGTTGGGGCAAGAGTGCAGGCTCCGATGATCACTAC	258
Db	121	CCCAAGAACGCGGGGCTGCAGTTGGGGCAAGAGTGCAGGCTCCGATGATCACTAC	180
Oy	259	CTGGGCGCGCATCAAGCGGGGCACTTCTCCAAGAGAGAGACACCATTATCAT	318
Db	181	CTGGGCGCGCATCAAGCGGGGCACTTCTCCAAGAGAGAGACACCATTATCAT	240
Oy	319	CTCCACGAGCTGCTTGGCAACAGGTGGTCCGCAATTGCCCGCAGGTGCCGGAGAGC	378
Db	241	CTCCACGAGCTGCTTGGCAACAGGTGGTCCGCAATTGCCCGCAGGTGCCGGAGAGC	300
Oy	379	GACAACGAGATCAAGAACTGTGGCAC-AACCACCTCAAGAAAGGCGCTCGATGGCGGC	437
Db	301	GACAACGAGATCAAGAACTGTGGCAC-AACCACCTCAAGAAAGGCGCTCGATGGCGGC	360
Oy	438	TCAGGGCGCTATCTCGCGCGAGCGCGGCAAGACACAAAGACCGAAGACGCGCAA	497
Db	361	TCAGGGCGCTATCTCGCGCGAGCGCGGCAAGACACAAAGACCGAAGACGCGCAA	420
Oy	498	GAAAGCAAGC	557
Db	421	GAAAGCAAGC	479
Oy	558	GATGACGAGGCTCTCGATGGAGCTGTGCGGTGGCGAGAGAGACGCGCAAGCGCGGATCAG	617
Db	480	GATGACGAGGCTCTCGATGGAGCTGTGCGGTGGCGAGAGAGACGCGCAAGCGCGGATCAG	539
Oy	618	CTGGGCGCTCGGCTCGGTGGCGCAAGAGAGAGCTCTTCACTTCGCGCTTCGAGGA	677

Db	540	CTGGCGCTCCGCGCTCCGCTGTGTGGCCGAAGAGAGAGCTCTTCACTCGGCTCCGAGGA	599
Oy	678	GTTCCAGATCGACGACAGCTTCTGTGTGGAGAGCGTGTGATGCCGCTGACGGGATACGA	737
Db	600	GTTCCAGATCGACGACAGCTTCTGTGTGGAGAGCGTGTGATGCCGCTGACGGGATACGA	659
Oy	738	CGTGTCATGTGAGCGCCGGCGAGCGCTTGTGTGGCGCGCATTCGCGCAGCATGAGACTA	797
Db	660	CGTGTCATGTGAGCGCCGGCGAGCGCTTGTGTGGCGCGCATTCGCGCAGCATGAGACTA	719
Oy	798	CTGGCTCGGAGAGTTCATGTGAGTCCGGCGAAGCGCAAGACTTGGCCGAGATCTAG	852
Db	720	CTGGCTCGGAGAGTTCATGTGAGTCCGGCGAAGCGCAAGACTTGGCCGAGATCTAG	774
RESULT 9			
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LOCUS			PLN 17-FEB-2002
DEFINITION	AF467733	Oryza sativa myb protein mRNA, complete cds.	
ACCESSION	AF467733	GI:18698671	
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
		Oryza sativa	
		Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
		Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP	
		clade; Ehrhartoideae; Oryzaceae; Oryza.	
		1 (baae 1 to 673)	
REFERENCE		Yao,Q., Peng,R., Xiong,A., Li,X. and Fan,H.	
AUTHORS		Submitted (14-JAN-2002) Bio-tech, Shanghai Academy of Agriculture	
TITLE		Science, Beid Road 2901, Shanghai 201106, China	
JOURNAL		Location/Qualifiers	
FEATURES			
source		1..673	
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		/db_xref="GI:18698672"	
		/translation="MGRAPCCEKXKGLKSPWTPEDKVLVNIORHGNMRLPKQA	
		GLKNGSCLRIMWIKRPDIKRGFSKEEDTIHHELIQMSAIARLPETDID	
		EIKVMVTHLKKRLDAPAGSHVAASGSKHKHKXKTRRSOPPPGRGVASRR"	
ORIGIN			
Query Match		45.5%; Score 546.4; DB 4; Length 673;	
Best Local Similarity		96.4%; Pred. No. 8,9e-126;	
Matches		623; Conservative 0; Mismatches 16; Indels 7; Gaps 6;	
Oy	2	AGCGCCTCCCTTCCAGAACACACAAACGCAAGAGACAGAGCAAGTTCAGATCAGAGCA	61
Db	2	AGCGCCTCCCTTCCAGAACACACAAACGCAAGAGAGACAGAGCAAGTTCAGATCAGAGCA	61
Oy	62	GGAAGAGACAGACATGTGGGAGAGGCTCTGTGTGGGAAAGATGGGGCTCAAGAAAG	121
Db	62	GGAAGAGACAGACATGTGGGAGAGGCTCTGTGTGGGAAAGATGGGGCTCAAGAAAG	121
Oy	122	GTCATGTAGCGCCGAGAGAGCAAGAGTCTCTGTGTGCCCATTCAGACGCGCAGCAGC	181
Db	122	GTCATGTAGCGCCGAGAGAGCAAGAGTCTCTGTGTGCCCATTCAGACGCGCAGCAGC	181
Oy	182	GCAATGTGCGCGCTTGCCTGCAAGCAAGCGGAGCTGCTGTTGGCGCAAGAGCTGCGGC	241
Db	182	GCAATGTGCGCGCTTGCCTGCAAGCAAGCGGAGCTGCTGTTGGCGCAAGAGCTGCGGC	241
Oy	242	TCCGATGATCAACTACTCTGTGCGCGCGGACATTAAGCGGGGCACTTCTTCAAGAGAGAG	301
Db	242	TCCGATGATCAACTACTCTGTGCGCGCGGACATTAAGCGGGGCACTTCTTCAAGAGAGAG	301

[illegible]

QY	314	TCATCTCCACGAGTGTGGCAAGAGTGTCCGCAATTTGGCCGCGAGTTGCCCGGGA	373
Db	232	TCGAGTGCACCGCTGCTCGGCAACAGATGCTCCGATTCGCCGCAAGCTCCGCGGA	291
QY	374	GGAACGACACGAGATCAAGAAAGTGTGGCAACCCACTCAAGAAAGCGCTGATGCGC	433
Db	292	GGAACGACACGAGATCAAGAAAGTGTGGCAACCCACTCAAGAAAGCGCTGATGCGCA	351
QY	434	CGGCTAAGGCGGTCTATGTTCGCGCGACGCGCGGCAAGAACCAAGAACCGGAAG----	489
Db	352	GCGCGACGAGACGACAAAGAAAGCGCGCGCGCAAGAACCGCGCGCGCGCGCGCG	411
QY	490	-----ACGCGCAAGA	499
Db	412	CGGCGCGCGCGCGGAGAAAGCGGACGCGCAAGTCAAGATGAGAAACCTCAACGCGCTCA	471
QY	500	AGCCAGCCG	559
Db	472	CGCCAGGCGGTGCG	531
QY	560	TGACGAGTTC---TGATGCGCTCTGCTGCGCGCGGACGACGCGCAACCGCGGATCA	616
Db	532	TGACGAGTTCGAGTTCGACCGCTCTGCGCGCGCGCGGACGACGCGCAACCGCGGATCA	591
QY	617	GCTCGGCGTCCGCGCTCGTGTGCGCGCAAGAGAGAGCT---CCTTCACTTCGCGCTTCCG	673
Db	592	GCTCGGCGTCCGCGCTCGTGTGCGCGCGCAAGAGAGAGCT---CCTTCACTTCGCGCTTCCG	651
QY	674	AGGAGTTCAGATCGACGACAGCTTGTGTGCGAGACGCTGTGATGCGCTGAGACG---	730
Db	652	AGGAGTTCAGATCGACGACAGCTTGTGTGCGAGACGCTGTGATGCGCTGAGACG---	711
QY	731	GGTGAACGCTGTCAGAGAGCGCGCGGAGCGCTTGTGCGCGCGCGCGCGCGCGCGAGCA	790
Db	712	TCAACGACGCTGTGATGAGAGCGCGCGGAGCGCGCTTGTGCGCGCGCGCGCGCGAGCA	765
QY	791	TGAGTACTGCTGCTCGAGTGTTCATGAGTCCGCGCG	826
Db	766	TGAGTACTGCTGCTCGAGTGTTCATGAGAGGCGCGCG	801
RESULT 12			
LOCUS	AK112056	1038 bp	mRNA linear
DEFINITION	Oryza sativa (japonica cultivar-group) cDNA clone:001-110-C03, full insert sequence.		
ACCESSION	AK112056		
VERSION	AK112056.1	GI:37988719	
KEYWORDS	FLI CDNA; oligo capping.		
SOURCE	Oryza sativa (japonica cultivar-group)		
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Bep clade; Ehrhartoideae; Oryzaceae; Oryza.		
REFERENCE	1		
AUTHORS	The Rice Full-length cDNA Consortium, National Institute of Agrobiological Sciences Rice Full-length cDNA Project Team; Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yasaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuka, K., Shishiki, T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group; Ootomo, Y., Murakami, K., Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y., Kuroseki, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, Q., Lu, M., Naitaka, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Nishikura, J., Ikeda, R., Ishibiki, J., Kawamata, M., Yoshimura, A., Miura, J., Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Matubara, K., RIKEN; Kawai, J., Carninci, P., Adachi, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashidume, W., Hayatsu, N., Imotani, K., Ishii, Y., Itoh, M., Saito, R., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Yoshino, M., and Hayashizaki, Y.		
TITLE	Collection, mapping, and annotation of over 28,000 cDNA clones from		

JOURNAL
PUBMED
REFERENCE
AUTHORS
japonica rice
Science 301 (5631), 376-379 (2003)
12869764

TITLE
JOURNAL
REFERENCE
AUTHORS
Unpublished
Rice full-length cDNA
3 (bases 1 to 1038)
Kikuchi, S.
Direct Submission
Submitted (12-SEP-2002) Shoshi Kikuchi, National Institute of Agrobiological Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression, 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan (E-mail:skikuchi@nias.affrc.go.jp, Tel:81-29-838-7007, Fax:81-29-838-7007)
This clone is one of the 32k full-length cDNA clones from japonica rice.

COMMENT
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ORIGIN

Query Match 27.2%; Score 326.6; DB 4; Length 1038;
 Best Local Similarity 71.0%; Pred. No. 1.1e-70;
 Matches 488; Conservative 0; Mismatches 169; Indels 30; Gaps .3;

ORIGIN

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 121 CATGGGAGGAGGAGGCTCCGCTGCTGCGAAGATGGGGCTCAAGAGGGGCGGTGGACCGCG 180
 137 AGGAGGACAAAGGCTCTCTGCTGCCCATCATCGAGCCGACCGGCAACTGGCGCGCC 196
 181 AGGAGGACAAAGATCTCTGCTGCCCATCATCGAGCCGACCGGCAACTGGCGCGCG 240
 197 TGGCCCAAGAGAGCGGGGCTGCTGCTGGGGCAAGAGCTGCCGGCTCCGGTGGATCACT 256
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 257 ACCGCGGCGGACATCAAGCGGGGCACTTCTCAAGAGAGAGAGACACCATCATCC 316
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 317 ATCTCCAGAGAGCTCTTGGCAACAGTGTCCGCAATTGGCCGACAGTTGCCCGGAGGA 376
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 481 CGTGTGCGGCGGAG 540
 494 CGAAG 553
 541 TGGCGGCTGCGAGATCGAGTTCGAGCCGAGCCGCTGCTGCGAGAGAGAGAGAGAG 600
 554 CGTGGGAG 613
 601 CCAGCAG 640
 614 TCAGCTCGGAG 673
 641 ----CTCGATGGGCTCTCTCGGAGATCAACAACAAGAGAGAGAGAGAGAGAGAG 693
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 694 AGGAGTTCAGATTCAG 753
 734 AGGAGTTCAGATTCAG 760
 754 CCGAGCTCGGAG 780

RESULT 13
 AX653760 672 bp DNA linear PAT 22-MAR-2003
 DEFINITION Sequence 3630 from Patent WO03000898.
 ACCESSION AX653760
 VERSION AX653760.1 GI:29156574
 KEYWORDS
 SOURCE Oryza sativa
 ORGANISM Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BBP
 clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
 AUTHORS Chang, H.S., Chen, W., Cooper, B., Glazebrook, J., Goff, S.A., Hou, Y.M.,
 Katagiri, F., Quan, S., Tao, Y., Whitcham, S., Xie, Z., Zhu, T. and Zou, G.
 TITLE Plant genes involved in defense against pathogens
 JOURNAL Patent: WO 03000898-A 3630 03-JAN-2003;
 Syngenta Participations AG (CH)
 FEATURES
 source Location/Qualifiers
 1..672

Query Match 23.6%; Score 284.2; DB 2; Length 672;
 Best Local Similarity 71.6%; Pred. No. 4.9e-60;
 Matches 386; Conservative 1; Mismatches 149; Indels 3; Gaps 1;

ORIGIN

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 1 ATGGGAGGAGGAGGCTCCGCTGCTGCGAAGATGGGGCTCAAGAGGGGCGGTGGACCGCG 60
 139 GAGGACAAAGTCTCTGCTGCCCATCATCGAGCCGACCGGCAACTGGCGCGCGCTG 198
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 361 TGTGCGGCGGAG 420
 496 AAG 555
 421 GCGGTGGAGATTCAG 480
 556 TCGGTGAG 614
 481 GACGACAGCTTCTGCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 539

RESULT 14
 AY178579 330 bp mRNA linear PLN 18-JAN-2003
 DEFINITION Lolium perenne R2R3 MYB protein MYB4 (Myb4) mRNA, partial cds.
 ACCESSION AY178579
 VERSION AY178579.1 GI:27802511
 KEYWORDS
 SOURCE Lolium perenne
 ORGANISM Lolium perenne
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BBP
 clade; Pooideae; Poaceae; Lolium.

REFERENCE
 AUTHORS Larsen, K.
 TITLE Cloning of MYB transcription factors expressed in stem tissue of
 perennial ryegrass
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 330)
 AUTHORS Larsen, K.
 TITLE Direct Submission
 JOURNAL Submitted (13-NOV-2002) Department of Crop Physiology and Soil
 Science, Danish Institute of Agricultural Sciences, Blichers Alle,
 Tjele DK-8830, Denmark
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ORIGIN

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Query Match      22.4%; Score 269.8; DB 4; Length 330;
Best Local Similarity 88.8%; Pred. No. 26-56;
Matches 292; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

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DB 61 GAGGACAGAGTCTCGTCGCGCCACATCCAGCGCCACGCGCAACTGGCGCGCTG 120
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DB 301 GACCAAGAGATCAAGAGCTGTGGACAC 329
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RESULT 15
OSMYB1084      1084 bp  mRNA  linear  PLN 18-APR-2005
LOCUS          O.sativa mRNA for myb factor, 1084 bp.
DEFINITION     Y11350
ACCESSION      Y11350
VERSION        Y11350.1 GI:1945278
KEYWORDS       myb gene.
SOURCE          Oryza sativa (japonica cultivar-group)
ORGANISM       Oryza sativa (japonica cultivar-group)
                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BIP
                clade; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE      1 (bases 1 to 1084)
AUTHORS        Solinas,G., Valle,G., Pandolfi,D. and Coraggio,I.
TITLE          The electronic Plant Gene Register
JOURNAL        Plant Physiol. 114 (2), 747-749 (1997)
PUBMED         9235602
REFERENCE      2 (bases 1 to 1084)
AUTHORS        Coraggio,I.
TITLE          Direct Submision
JOURNAL        Submitted (18-FEB-1997) I. Coraggio, CNR, Istituto Biosintesi
                Vegetali, Via Bassini 15, Milano, 20131, ITALY
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ORIGIN

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Query Match      22.4%; Score 269.2; DB 4; Length 1084;
Best Local Similarity 70.1%; Pred. No. 2.8e-56;
Matches 380; Conservative 0; Mismatches 153; Indels 9; Gaps 1;

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DB 365 GCCTCCACAACCTCCTCGGCAACAGGTGTCGCAATTGCGCGAGTGGCGGAGAG 424
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QY 377 CGGACAGAGATCAAGAGCTGTGGACACCCACTTCAAGAGCGCTCGATG----- 430
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DB 425 CTGACCAAGAGATCAAGAGCTGTGGACACCTCAAGAGAGAGCTGAGCGAAGAC 484
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QY 431 ---CGCGGCTCAGGCGGCTCATGTGCGGCGAGCGCGCAAGAGCAAGAGCGGA 487
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DB 665 AC 666
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Search completed: June 25, 2006, 14:14:27
Job time : 6813 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: June 23, 2006, 23:55:18 ; Search time 199 Seconds
(without alignments)
590.475 Million cell updates/sec

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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1153	84.3	257	ADA48652	Ada48652 Rice prot
2	1153	84.3	257	ABM90166	Abm90166 Rice abio
3	827.5	60.5	258	ABJ10408	Abj10408 Myb-relat
4	827.5	60.5	258	ADH50100	Adh50100 Rice Myb-
5	799.5	58.4	257	AA654568	Aag54568 Zea mays
6	799.5	58.4	309	AA654568	Aag54568 Zea mays
7	762.5	55.7	162	ADA48106	Ada48106 Rice prot
8	762.5	55.7	162	ABM85964	Abm85964 Rice abio
9	747.5	54.6	248	AA654570	Aag54570 Zea mays
10	684	50.0	277	AD142106	Ad142106 Plant tra
11	669.5	48.9	278	AAW17811	Aaw17811 Tobacco M
12	661.5	48.4	385	AA641251	Aag41251 Arabidops
13	661.5	48.4	285	ADN72611	Adn72611 Thale cre
14	661.5	48.4	304	ADX91441	Adx91441 Plant ful
15	658	48.1	313	ADX71586	Adx71586 Plant ful
16	641.5	46.9	260	ADW17408	Adw17408 Eucalyptu
17	640	46.8	273	AAE01914	Aae01914 Arabidops
18	640	46.8	273	AAE01930	Aae01930 Arabidops
19	640	46.8	273	AAE02542	Aae02542 A. thalia
20	640	46.8	273	ADA15585	Ada15585 A. thalia
21	640	46.8	273	ABO43123	AbO43123 A. thalia
22	640	46.8	273	ADD55700	Add55700 Thalecres
23	640	46.8	273	ADD30744	Add30744 Plant yle

24	640	46.8	273	8	AD141577	Ad141577 Plant tra
25	640	46.8	273	8	AD143515	Ad143515 Plant tra
26	640	46.8	273	8	AD003341	Ad003341 Thalecres
27	640	46.8	273	8	AD001751	Ad001751 Thalecres
28	640	46.8	273	8	AD001743	Ad001743 Thalecres
29	640	46.8	276	9	AD267575	Ad267575 Arabidops
30	628.5	45.9	246	5	AEC91871	Aec91871 Thale cre
31	626.5	45.8	139	5	ABJ10425	Abj10425 Myb-relat
32	626.5	45.8	139	8	ADH50134	Adh50134 Rice Myb-
33	623.5	45.6	246	8	AD001703	Ad001703 Thalecres
34	608	44.4	249	3	AA630515	Aag30515 Arabidops
35	606.5	44.3	276	3	AA641252	Aag41252 Arabidops
36	601	43.9	249	4	AAE02557	Aae02557 A. thalia
37	601	43.9	249	6	ADA15467	Ada15467 A. thalia
38	601	43.9	249	8	AD002409	Ad002409 Thalecres
39	597	43.6	249	3	AA626239	Aag626239 Arabidops
40	593	43.3	264	8	ADX94416	Adx94416 Plant ful
41	592	43.3	250	9	ADW17378	Adw17378 Eucalyptu
42	584	42.7	386	9	ADW17784	Adw17784 Pinus rad
43	582	42.5	122	7	ABO43148	AbO43148 A. thalia
44	582	42.5	122	7	ADD55856	Add55856 Thalecres
45	563	41.2	481	9	ADW18468	Adw18468 Pinus rad

ALIGNMENTS

RESULT 1	ADA48652	ADA48652 standard; protein; 257 AA.
XX	ADA48652;	
AC	ADA48652;	
XX		
DT	20-NOV-2003 (first entry)	
XX		
DE	Rice protein conferring disease resistance in plants.	
XX		
KW	disease resistance; pathogen tolerance; plant pathogen; plant; rice.	
OS	Oryza sativa.	
XX		
PN	MO2003000906-A2.	
XX		
PD	03-JUN-2003.	
XX		
PF	21-JUN-2002; 2002MO-IB002453.	
XX		
PR	22-JUN-2001; 2001US-0300112P.	
XX		
PR	26-SEP-2001; 2001US-0352277P.	
XX		
PR	22-MAR-2002; 2002US-0366535P.	
XX		
PA	(SYGN) SYNGENTA PARTICIPATIONS AG.	
XX		
PI	Glazebrook J, Briggs S, Cooper B, Goff SA, Moughamer T;	
XX	Katagiri F, Kreps J, Provart N, Riecke D, Zhu T;	
PI	WPI; 2003-184052/18.	
DR	N-PSDB; ADA48651.	
XX		
PT	New polynucleotide comprising a plant nucleotide sequence having an open	
XX	reading frame that encodes a polypeptide associated with disease	
PT	resistance, useful for conferring resistance or tolerance to a plant	
XX	pathogen.	
PS	claim 10; SEQ ID NO 722; 299pp; English.	
XX		
CC	The invention relates to a novel isolated polynucleotide comprising a	
CC	plant nucleotide sequence having an open reading frame that encodes a	
CC	polypeptide associated with disease resistance or its fragment having	
CC	substantially the same activity as the full-length polypeptide. The	
CC	polynucleotide of the invention is useful for conferring resistance or	
CC	tolerance to a plant pathogen. The present sequence represents a protein	
CC	conferring disease resistance used in the invention.	

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XX      SQ      Sequence 257 AA;
Query Match      84.3%; Score 1153; DB 6; Length 257;
Best Local Similarity 84.1%; Pred. No. 6.4e-103;
Matches 222; Conservative 11; Mismatches 17; Indels 14; Gaps 3;

QY      1 MGRAPCCCKMGLKKGPWTPPEEDKVLVAHIQRHGHGHWRLALPQAGLLRCGKSCRRLRWNY 60
      |||
      1 MGRAPCCCKMGLKKGPWTPPEEDKVLVAHIQRHGHGHWRLALPQAGLLRCGKSCRRLRWNY 60
DB      61 LRPDIKRGNFSKEEDTIIHLHELGNRWSAIAARLPGRTDNEIKNVWHTHLKKRLDAPA 120
      |||
      61 LRPDIKRGNFSKEEDTIIHLHELGNRWSAIAARLPGRTDNGIKNVH-----NPPQ 113
DB      121 QCGHVAAG---GKHKKPKSAKKPAAA--AAPASPERASASSVTSSMASSVAEE 173
      |||
      114 EAPRCAGSGRSGRGERROAEOAEEREEASRRRRPPASPERASASSVTSSMASSVAEE 173
QY      174 HGNAGISSASASVCAKEESSFTSASREFOIDSFMSSETLMPLDGYDVSMERGDAFVAP 233
      |||
      174 HGNAGISSASASVCAKEESSFTSASEEFOIDSFMSSETLMPLDGYDVSMERGDAFVAP 233
DB      234 SADMDYWLGVFMESGEAQLDLPQI 257
QY      234 SADMDYWLGVFMESGEAQLDLPQI 257
DB      234 SADMDYWLGVFMESGEAQLDLPQI 257

RESULT 2
ABM90166
ID      ABM90166 standard; protein; 257 AA.
XX
XX      ABM90166;
XX
DT      02-JUN-2005 (first entry)
XX
DE      Rice abiotic stress responsive polypeptide SEQ ID NO:8888.
XX
KM      abiotic stress tolerance; transgenic plant; plant; cereal; agriculture.
XX
OS      Oryza sativa.
XX
PN      WO2003008540-A2.
XX
PD      30-JAN-2003.
XX
PF      21-JUN-2002; 2002WO-US019668.
XX
PR      22-JUN-2001; 2001US-0300112P.
XX      24-AUG-2001; 2001US-0314662P.
XX      26-SEP-2001; 2001US-0325277P.
XX      21-NOV-2001; 2001US-0332132P.
XX
PA      (SYGN ) SYNGENTA PARTICIPATIONS AG.
XX
PI      Kreps J, Briggs SP, Cooper B, Glazebrook J, Goff SA, Katagiri F,
PI      Moughamer T, Provart N, Rieke D, Zhu T;
XX
DR      WPI; 2003-248011/24.
XX
PT      New stress-responsive nucleic acid, useful for altering the
PT      responsiveness of a plant, e.g. cereal, to an abiotic stress such as cold
PT      stress, salt stress or osmotic stress.
XX
PS      Claim 1, SEQ ID NO 8888, 89pp; English.
XX
CC      The invention relates to novel abiotic stress responsive polynucleotides
CC      and polypeptides. Also disclosed are vectors, expression cassettes, host
CC      cells, and plants containing such polynucleotides. Also disclosed are
CC      methods for using the polynucleotides and polypeptides to alter the
CC      responsiveness of a plant to abiotic stress. The invention is useful in
CC      agriculture. The nucleic acid is useful for determining whether a test
CC      plant has been exposed to an abiotic stress condition. It is also useful

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CC      for selecting an agent that alters abiotic stress regulated
CC      polynucleotide expression in a plant cell, and to identify a homolog or
CC      ortholog to an abiotic stress responsive polynucleotide. The nucleic acid
CC      molecule and the polypeptide encoded by it are useful in altering the
CC      responsiveness of a plant to an abiotic stress, such as cold stress, salt
CC      stress, osmotic stress or any of their combinations. The present sequence
CC      is used in the exemplification of the invention

XX      SQ      Sequence 257 AA;
Query Match      84.3%; Score 1153; DB 7; Length 257;
Best Local Similarity 84.1%; Pred. No. 6.4e-103;
Matches 222; Conservative 11; Mismatches 17; Indels 14; Gaps 3;

QY      1 MGRAPCCCKMGLKKGPWTPPEEDKVLVAHIQRHGHGHWRLALPQAGLLRCGKSCRRLRWNY 60
      |||
      1 MGRAPCCCKMGLKKGPWTPPEEDKVLVAHIQRHGHGHWRLALPQAGLLRCGKSCRRLRWNY 60
DB      61 LRPDIKRGNFSKEEDTIIHLHELGNRWSAIAARLPGRTDNEIKNVWHTHLKKRLDAPA 120
      |||
      61 LRPDIKRGNFSKEEDTIIHLHELGNRWSAIAARLPGRTDNGIKNVH-----NPPQ 113
DB      121 QCGHVAAG---GKHKKPKSAKKPAAA--AAPASPERASASSVTSSMASSVAEE 173
      |||
      114 EAPRCAGSGRSGRGERROAEOAEEREEASRRRRPPASPERASASSVTSSMASSVAEE 173
QY      174 HGNAGISSASASVCAKEESSFTSASREFOIDSFMSSETLMPLDGYDVSMERGDAFVAP 233
      |||
      174 HGNAGISSASASVCAKEESSFTSASEEFOIDSFMSSETLMPLDGYDVSMERGDAFVAP 233
DB      234 SADMDYWLGVFMESGEAQLDLPQI 257
QY      234 SADMDYWLGVFMESGEAQLDLPQI 257
DB      234 SADMDYWLGVFMESGEAQLDLPQI 257

RESULT 3
ABJ10408
ID      ABJ10408 standard; protein; 258 AA.
XX
XX      ABJ10408;
XX
DT      21-NOV-2002 (first entry)
XX
DE      Myb-related transcription factor protein SEQ ID No 4.
XX
KM      Myb; Myb-related transcription factor; plant; transgenic plant.
XX
OS      Oryza sativa.
XX
PN      US2002066120-A1.
XX
PD      30-MAY-2002.
XX
PF      19-NOV-1999; 99US-00443704.
XX
PR      20-NOV-1998; 98US-0109294P.
XX
PA      (CAHO/) CAHOON R E.
PA      (LITUZ/) LITU Z.
PA      (ODEL/) ODEL J T.
PA      (RAFA/) RAFALSKI J A.
PA      (SHIJ/) SHI J.
PA      (WENG/) WENG Z.
XX
PI      Cahoon RE, Liu Z, Odell JT, Ratajski JA, Shi J, Weng Z;
XX
XX      WPI; 2002-556780/59.
XX      N-PSDB; ABR08112.
XX
PT      Novel isolated polynucleotide useful for obtaining a nucleic acid
PT      fragment encoding a Myb-related transcription factor polypeptide.
XX
XX      Claim 10; Page 15-16; 51pp; English.

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XX The invention relates to a novel isolated polynucleotide comprising a
CC first nucleotide encoding a polypeptide of 217, 120, or 268 amino acids
CC that has 85%, 95%, or 96% identity based on the Clustal method of
CC alignment when compared to a polypeptide selected from Myb polypeptides
CC sequences of 128, 258, or 268 amino acids fully defined in the
CC specification, or a second nucleotide sequence comprising the complement
CC of the first nucleotide. The isolated polynucleotide is useful for
CC obtaining a nucleic acid fragment encoding an Myb-related transcription
CC factor polypeptide by using it to probe cDNA or genomic libraries. A
CC nucleic acid fragment obtained using the isolated polynucleotide is
CC useful to isolate cDNAs and genes encoding homologous proteins from the
CC same or other plant species. The nucleic acid fragment is also useful to
CC create transgenic plants in which the Myb-like protein is present at
CC higher or lower levels than normal or in cell types. This sequence
CC represents the protein of an Myb-related transcription factor of the
CC invention

SQ Sequence 258 AA;

Query Match 60.5%; Score 827.5; DB 5; Length 258;
Best Local Similarity 62.1%; Pred. No. 2.3e-71;
Matches 169; Conservative 29; Mismatches 45; Indels 29; Gaps 8;

QY 1 MGRAPCCCKMGLKKGWTPBEDKVLVAHIQRHGHGWRALPRQAGLLRCGKSCRLWIMY 60
DB 1 MGRAPCCCKMGLKKGWTPBEDKVLVAHIQRHGHGWRALPRQAGLLRCGKSCRLWIMY 60
QY 61 LRPDIRKGNFSEEDTIIHLHELGNRMSAIAARLPGRTDNEIKVWHTLKKRLDAPA 120
DB 61 LRPDIRKGNFSEEDTIIHLHELGNRMSAIAARLPGRTDNEIKVWHTLKKRLDAPA 120
QY 121 OGCHVAAGCGKKHKKPKSAKKPAAAAA-----PASPERASSSVTSSMASSVAEEH 174
DB 121 SSGREAAA-----PKKATKKAATAVAIDVPTTVSPSQSLSTTTT-----SAATTEBY 171
QY 175 GNAGISASASVCAKESSFTSASEFOIDDSFWSFTLSMPIDGYVSM-----PGDAF 229
DB 175 GNAGISASASVCAKESSFTSASEFOIDDSFWSFTLSMPIDGYVSM-----PGDAF 229
QY 230 VAPPSA---DDM-DYWLGVFMESGEAODLPQI 257
DB 227 GASPSSSNDMDDFWLKLFIAQGQNLQPI 258

RESULT 4

ADH50100

ID ADH50100 standard; protein; 258 AA.

XX ADH50100;

XX 25-MAR-2004 (first entry)

XX Rice Myb-related transcription factor #1.

XX Myb-related transcription factor; transcriptional regulation; plant;
XX gene regulation; rice.

XX Oryza sativa.

XX US2002187539-A1.

XX 12-DEC-2002.

XX 05-DEC-2001; 2001US-00008118.

XX 20-NOV-1998; 98US-0109294P.

XX 19-NOV-1999; 99US-00443704.

XX (CAHO/) CAHOON R E.

XX (WENG/) WENG Z.

XX Cahoon RE, Weng Z;

XX WPI; 2004-059062/06.
DR N-PSDB; ADH50099.
XX A new isolated plant nucleic acid fragments encoding a Myb-related
PT transcription factor in plants and seeds, are useful to control gene
PT expression.

PS Claim 10; SEQ ID NO 4; 53pp; English.

XX The invention comprises the amino acid and coding sequences of Myb-
CC related transcription factors - these proteins are involved in
CC transcriptional regulation in plants. The DNA and protein sequences of
CC the invention may be used to facilitate studies to better understand gene
CC regulation in plants and provide genetic tools to enhance or otherwise
CC alter the expression of genes controlled by Myb-related transcription
CC factors. The present amino acid sequence represents an Myb-related
CC transcription factor of the invention.

SQ Sequence 258 AA;

Query Match 60.5%; Score 827.5; DB 8; Length 258;
Best Local Similarity 62.1%; Pred. No. 2.3e-71;
Matches 169; Conservative 29; Mismatches 45; Indels 29; Gaps 8;

QY 1 MGRAPCCCKMGLKKGWTPBEDKVLVAHIQRHGHGWRALPRQAGLLRCGKSCRLWIMY 60
DB 1 MGRAPCCCKMGLKKGWTPBEDKVLVAHIQRHGHGWRALPRQAGLLRCGKSCRLWIMY 60
QY 61 LRPDIRKGNFSEEDTIIHLHELGNRMSAIAARLPGRTDNEIKVWHTLKKRLDAPA 120
DB 61 LRPDIRKGNFSEEDTIIHLHELGNRMSAIAARLPGRTDNEIKVWHTLKKRLDAPA 120
QY 121 OGCHVAAGCGKKHKKPKSAKKPAAAAA-----PASPERASSSVTSSMASSVAEEH 174
DB 121 SSGREAAA-----PKKATKKAATAVAIDVPTTVSPSQSLSTTTT-----SAATTEBY 171
QY 175 GNAGISASASVCAKESSFTSASEFOIDDSFWSFTLSMPIDGYVSM-----PGDAF 229
DB 175 GNAGISASASVCAKESSFTSASEFOIDDSFWSFTLSMPIDGYVSM-----PGDAF 229
QY 230 VAPPSA---DDM-DYWLGVFMESGEAODLPQI 257
DB 227 GASPSSSNDMDDFWLKLFIAQGQNLQPI 258

RESULT 5

AAG54569

ID AAG54569 standard; protein; 257 AA.

XX AAG54569;

XX 18-OCT-2000 (first entry)

XX Zea mays protein fragment SEQ ID NO: 69592.

XX Protein identification; signal transduction pathway; metabolic pathway;
XX hybridization assay; genetic mapping; gene expression control; promoter;
XX termination sequence; corn.

XX Zea mays subsp. mays.

XX EP1033405-A2.

XX 06-SEP-2000.

XX 25-FEB-2000; 2000EP-00301439.

XX 25-FEB-1999; 99US-0121825P.

XX 05-MAR-1999; 99US-0123180P.

XX 09-MAR-1999; 99US-0123548P.

XX 23-MAR-1999; 99US-0125788P.

XX 25-MAR-1999; 99US-0126264P.

PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 23-APR-1999; 99US-0130891P.
PR 28-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
PR 30-APR-1999; 99US-0132407P.
PR 04-MAY-1999; 99US-0132484P.
PR 05-MAY-1999; 99US-0132485P.
PR 06-MAY-1999; 99US-0132486P.
PR 06-MAY-1999; 99US-0132487P.
PR 07-MAY-1999; 99US-0132863P.
PR 11-MAY-1999; 99US-0134256P.
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PR 14-MAY-1999; 99US-0134221P.
PR 14-MAY-1999; 99US-0134370P.
PR 18-MAY-1999; 99US-0134768P.
PR 19-MAY-1999; 99US-0134941P.
PR 20-MAY-1999; 99US-0135124P.
PR 21-MAY-1999; 99US-0135353P.
PR 24-MAY-1999; 99US-0135629P.
PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
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PR 08-JUN-1999; 99US-0138094P.
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PR 10-JUN-1999; 99US-0138847P.
PR 14-JUN-1999; 99US-0139119P.
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PR 18-JUN-1999; 99US-0139459P.
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PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139462P.
PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139500P.
PR 18-JUN-1999; 99US-0139763P.
PR 21-JUN-1999; 99US-0139817P.
PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140353P.
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PR 24-JUN-1999; 99US-0140695P.
PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-014091P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142977P.
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PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.
PR 16-JUL-1999; 99US-0144086P.

PR 19-JUL-1999; 99US-0144325P.
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PR 22-JUL-1999; 99US-0145085P.
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PR 22-JUL-1999; 99US-0145192P.
PR 23-JUL-1999; 99US-0145145P.
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PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145915P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
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PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147302P.
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PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147415P.
PR 09-AUG-1999; 99US-0147493P.
PR 09-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148319P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.
PR 13-AUG-1999; 99US-0148684P.
PR 16-AUG-1999; 99US-0149368P.
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PR 27-AUG-1999; 99US-0151066P.
PR 27-AUG-1999; 99US-0151080P.
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PR 31-AUG-1999; 99US-0151433P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153788P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0156589P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158023P.
PR 08-OCT-1999; 99US-0158232P.

PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0158293P.
PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
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PR 14-OCT-1999; 99US-0159637P.
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PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
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PR 21-OCT-1999; 99US-0160770P.
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PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
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PR 25-OCT-1999; 99US-0161404P.
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PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161820P.
PR 28-OCT-1999; 99US-0161992P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 58.4%; Score 799.5; DB 3; Length 257;

Best Local Similarity 58.8%; Pred. No. 1,2e-68; Matches 160; Conservative 30; Mismatches 51; Indels 31; Gaps 8;

QY 1 MGRAPCECEMGLKCGPMTPEEDKVLVAH;ORHCGNMRALPKQAGLRGCKSGLRWINY 60
DB 1 MGRSCECEMGLKCGPMTPEEDKVLVAH;ERHCHSWRALPKQAGLRGCKSGLRWINY 60
QY 61 LRPDIKRGNFSKEEDTIIHLHLLGNRWSAIAARLPRTDNEIKVWHTLKKRLD-AP 119
DB 61 LRPDIKRGNFSKEEDTIIHLHLLGNRWSAIAARLPRTDNEIKVWHTLKKRLD-AP 120
QY 120 AGCGHVAAGCGKKKKPKAKKPAALAAAP-PPSPERSAS--SSVTESSAASVAEE 173
DB 121 AS---QQAARKRPYKKQOPPEPVYALKEPTGAVPVSPERSSTTTSTTADYSAAS 177
QY 174 HGNAGISASASVCAKESSSFTSASEPQIDDSFMSSETISM--PLDGYDVSMRPGDA--- 228
DB 178 LENAG-----DSFTSEEDYXQIDDSFMSSETLAMTTTVSFESGVQQAAGSFG 224
QY 229 -FVAAPPSA--DDMDYVLGVFMESGEAODLPQI 257
DB 225 KSAAPPSTNDMDPWLKLFMQASDWMQNPQI 256

RESULT 6

AAG54568
ID AAG54568 standard; protein; 309 AA.

AC AAG54568;
XX

DT 18-OCT-2000 (first entry)
XX

DE Zee maye protein fragment SEQ ID NO: 69591.
XX

XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KM termination sequence; corn.

XX Zea maye subsp. maye.
OS

XX Zea maye subsp. maye.
XX

PN EPI03J405-A2.
XX

PD 06-SEP-2000.
XX 25-FEB-2000; 200EP-00301439.
XX 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 23-APR-1999; 99US-0130891P.
PR 28-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
PR 30-APR-1999; 99US-0132407P.
PR 04-MAY-1999; 99US-0132484P.
PR 05-MAY-1999; 99US-0132485P.
PR 06-MAY-1999; 99US-0132486P.
PR 06-MAY-1999; 99US-0132487P.
PR 07-MAY-1999; 99US-0132863P.
PR 11-MAY-1999; 99US-0134256P.
PR 14-MAY-1999; 99US-0134218P.
PR 14-MAY-1999; 99US-0134219P.
PR 14-MAY-1999; 99US-0134221P.
PR 18-MAY-1999; 99US-0134770P.
PR 19-MAY-1999; 99US-0134941P.
PR 20-MAY-1999; 99US-0135124P.
PR 21-MAY-1999; 99US-0135333P.
PR 24-MAY-1999; 99US-0135629P.
PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
PR 10-JUN-1999; 99US-0138847P.
PR 14-JUN-1999; 99US-0139119P.
PR 16-JUN-1999; 99US-0139452P.
PR 17-JUN-1999; 99US-0139492P.
PR 18-JUN-1999; 99US-0139454P.
PR 18-JUN-1999; 99US-0139455P.
PR 18-JUN-1999; 99US-0139456P.
PR 18-JUN-1999; 99US-0139457P.
PR 18-JUN-1999; 99US-0139458P.
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PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161932P.
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Query Match 58.4%; Score 799.5; DB 3; Length 309;
Best Local Similarity 58.8%; Pred. No. 1,5e-68;
Matches 160; Conservative 30; Mismatches 51; Indels 31; Gaps 8;

QY 1 MGRAPCCCKMGKLPMTPEEDKVLVAHIORHGNWRLPKQAGILRCGSKCRUMINY 60
DB 53 MGRSPCCCKMGKRPWTAEDRIIVAVHERHGNWRLPKQAGILRCGSKCRUMINY 112
QY 61 LRPDIKGNFSKEEDTIIHHELLGNFMSAIAARLPGRTDNEIKVWHTLKKRID-AP 119
DB 113 LRPDIKGNFSKEEDAIIOHQLGNFMSAIAARLPGRTDNEIKVWHTLKKRIDLEPKP 172
QY 120 AQCCHVAASGCKKHKPKSAKKPAALAAAP---PASPERAS--SVTESSMASSVAE 173
DB 173 AS--QAPKPKKPKTKQPPQPEPVTALEGPTGAVSPERSSTTTSTTADYASASS 229
QY 174 HGNAGISSASAVCAKESSEFTSASEFQIDDSFMSSETLSM--PLDGYDVSMEPGDA-- 228
DB 230 LENAG-----DSFTSEEDYQIDDSFMSSETLAWTTTSDYSPSSGQQAEGSGC 276
QY 229 -FVAPPSA--DDMDYVLGVFMESGEAODLPOT 257
DB 277 KSAAPPSSSTNDMDFMFLKLFMQASDMQNLPOI 308

RESULT 7
ADA48106
ID ADA48106 standard; protein; 162 AA.
XX
AC ADA48106;
XX
DT 20-NOV-2003 (first entry)
XX
DE Rice protein conferring disease resistance in plants.

XX disease resistance; pathogen tolerance; plant pathogen; plant; rice.
XX
XX Oryza sativa.
OS
XX WO2003000906-A2.
XX
XX 03-JAN-2003.
XX
XX 21-JUN-2002; 2002WO-1B002453.
XX
XX 22-JUN-2001; 2001US-0300112P.
XX
XX 26-SEP-2001; 2001US-0352277P.
XX
XX 22-MAR-2002; 2002US-0366535P.
XX
XX (SYGN) SYNGENTA PARTICIPATIONS AG.
XX
XX Glazebrook J, Briggs S, Cooper B, Goff SA, Moughamer T,
XX Katagiri F, Kreps J, Provart N, Riecke D, Zhu T;
XX WPI; 2003-184052/18.
XX
XX N-PSDB; ADA48105.
XX
XX New polynucleotide comprising a plant nucleotide sequence having an open
XX reading frame that encodes a polypeptide associated with disease
XX resistance, useful for conferring resistance or tolerance to a plant
XX pathogen.
XX
XX Claim 10; SEQ ID NO 176; 299BP; English.
XX
XX The invention relates to a novel isolated polynucleotide comprising a
XX plant nucleotide sequence having an open reading frame that encodes a
XX polypeptide associated with disease resistance or its fragment having
XX substantially the same activity as the full-length polypeptide. The
XX polynucleotide of the invention is useful for conferring resistance or
XX tolerance to a plant pathogen. The present sequence represents a gene
XX conferring disease resistance used in the invention.
XX
XX
SQ Sequence 162 AA;
Query Match 55.7%; Score 762.5; DB 6; Length 162;
Best Local Similarity 90.6%; Pred. No. 2.3e-65;
Matches 145; Conservative 2; Mismatches 8; Indels 5; Gaps 3;
QY 1 MGRAPCEKMGKKGWTPBEDKVLVAHIQRHGHGWRALPKQ-AGLRCGSCRLRWIN 59
DB 1 MGRAPCEKMGKKGWTPBEDKVLVAHIQRHGHGWRALPKQAGLRCGSCRLRWIN 60
QY 60 YLRPDIKRGNFSEEDDTIIHLHELLGN-RMSAIAARLPGRDNEIKVMHTLKKRLDA 118
DB 61 YLRPDIKRGNFSEEDDTIIHLHELLGNRWSAIAARFGRDNGIKVMHTLKKRLDA 120
QY 119 PAOGGHVAASGGKHKHKKPSAKKPAAPAAA---PPASPER 155
DB 121 PAOGGHVAASGGKHKHKKPSAKKPAAPAADGRRRRPSPGR 160
RESULT 8
ABM85964
ID ABM85964 standard; protein; 162 AA.
XX
XX ABM85964;
AC
XX
XX 02-JUN-2005 (first entry)
DT
XX
XX Rice abiotic stress responsive polypeptide SEQ ID NO:4210.
DE
XX
XX abiotic stress tolerance; transgenic plant; plant; cereal; agriculture.
XX
XX Oryza sativa.
OS
XX
XX WO2003008540-A2.
XX
XX
XX

PD 30-JAN-2003.
XX
XX 21-JUN-2002; 2002WO-US019668.
XX
XX 22-JUN-2001; 2001US-0300112P.
XX
XX 24-AUG-2001; 2001US-0314662P.
XX
XX 26-SEP-2001; 2001US-0325277P.
XX
XX 21-NOV-2001; 2001US-0332132P.
XX
XX (SYGN) SYNGENTA PARTICIPATIONS AG.
XX
XX Kreps J, Briggs SP, Cooper B, Glazebrook J, Goff SA, Katagiri F,
XX Moughamer T, Provart N, Riecke D, Zhu T;
XX WPI; 2003-248011/24.
XX
XX New stress-responsive nucleic acid, useful for altering the
XX responsiveness of a plant, e.g. cereal, to an abiotic stress such as cold
XX stress, salt stress or osmotic stress.
XX
XX Claim 1; SEQ ID NO 4210; 89pp; English.
XX
XX The invention relates to novel abiotic stress responsive polynucleotides
XX and polypeptides. Also disclosed are vectors, expression cassettes, host
XX cells, and plants containing such polynucleotides. Also disclosed are
XX methods for using the polynucleotides and polypeptides to alter the
XX responsiveness of a plant to abiotic stress. The invention is useful in
XX agriculture. The nucleic acid is useful for determining whether a test
XX plant has been exposed to an abiotic stress condition. It is also useful
XX for selecting an agent that alters abiotic stress regulated
XX polynucleotide expression in a plant cell, and to identify a homolog or
XX ortholog to an abiotic stress responsive polynucleotide. The nucleic acid
XX molecule and the polypeptide encoded by it are useful in altering the
XX responsiveness of a plant to an abiotic stress, such as cold stress, salt
XX stress, osmotic stress or any of their combinations. The present sequence
XX is used in the exemplification of the invention
XX
XX
SQ Sequence 162 AA;
Query Match 55.7%; Score 762.5; DB 7; Length 162;
Best Local Similarity 90.6%; Pred. No. 2.3e-65;
Matches 145; Conservative 2; Mismatches 8; Indels 5; Gaps 3;
QY 1 MGRAPCEKMGKKGWTPBEDKVLVAHIQRHGHGWRALPKQ-AGLRCGSCRLRWIN 59
DB 1 MGRAPCEKMGKKGWTPBEDKVLVAHIQRHGHGWRALPKQAGLRCGSCRLRWIN 60
QY 60 YLRPDIKRGNFSEEDDTIIHLHELLGN-RMSAIAARLPGRDNEIKVMHTLKKRLDA 118
DB 61 YLRPDIKRGNFSEEDDTIIHLHELLGNRWSAIAARFGRDNGIKVMHTLKKRLDA 120
QY 119 PAOGGHVAASGGKHKHKKPSAKKPAAPAAA---PPASPER 155
DB 121 PAOGGHVAASGGKHKHKKPSAKKPAAPAADGRRRRPSPGR 160
RESULT 9
AAG54570
ID AAG54570 standard; protein; 248 AA.
XX
XX AAG54570;
AC
XX
XX 18-OCT-2000 (first entry)
DT
XX
XX Zea mays protein fragment SEQ ID NO: 69593.
DE
XX
XX Protein identification; signal transduction pathway; metabolic pathway;
XX hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence; corn.
XX
XX Zea mays subsp. mays.
OS
XX
XX EP1033405-A2.
XX
XX
XX

XX 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-00301439.
XX
PR 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
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PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.
PR 16-JUL-1999; 99US-0144086P.
PR 19-JUL-1999; 99US-0144325P.
PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.

PR 20-JUL-1999; 99US-0144352P.
PR 20-JUL-1999; 99US-0144632P.
PR 20-JUL-1999; 99US-0144844P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
PR 21-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145085P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145192P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 02-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 05-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.
PR 06-AUG-1999; 99US-0147360P.
PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 09-AUG-1999; 99US-0147493P.
PR 09-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148319P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.
PR 13-AUG-1999; 99US-0148684P.
PR 16-AUG-1999; 99US-0149368P.
PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149426P.
PR 20-AUG-1999; 99US-0149722P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
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PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-SEP-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
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PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155139P.
PR 24-SEP-1999; 99US-0155486P.
PR 28-SEP-1999; 99US-0155659P.
PR 29-SEP-1999; 99US-0155658P.
PR 04-OCT-1999; 99US-0155596P.
PR 05-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157173P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
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PR 13-OCT-1999; 99US-0158294P.
PR 13-OCT-1999; 99US-0158295P.
PR 14-OCT-1999; 99US-0158329P.
PR 14-OCT-1999; 99US-0158330P.

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PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0153637P.
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PR 18-OCT-1999; 99US-0155984P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161922P.
PR 28-OCT-1999; 99US-0161933P.
PR 29-OCT-1999; 99US-0162142P.

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Query Match 48.4%; Score 661.5; DB 3; Length 285;
 Best Local Similarity 49.0%; Pred. No. 3.2e-55;
 Matches 146; Conservative 25; Mismatches 66; Indels 61; Gaps 6;

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OY 1 MGRAPCCCKMGLKKGPMTPBEDKVLVAH1QRHGNWRALPRQAGILRCGKSCRLRWNY 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 MGRAPCCCKMGLKKGPMTPBEDQILVSFLNHGSHWRALPRQAGILRCGKSCRLRWNY 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 61 LRPDIKRGNFSEEDTTIHLHELGNRWSAIAALPRTDNEIKVWHTHLKKRLDAPA 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 LRPDIKRGNFTEEBDAIISLHQILGNRWSAIAAKLPRTDNEIKVWHTHLKKRLE-DY 119
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 121 OCGHVAASGGKHKPKSAKKPAAAAAAPSPERSASSVTESSWASSVAEHNAGIS 180
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 120 QPAKPKTSNKKKGTTPKS-----ESVITSSNSTRESSELAIS---SNPSGES 163
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 181 SASASVCAKESSFTSASEE-----FOIDSPWSET 211
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 164 LFTSPSTSEVSMTLISHDGYSEINMNDKPGDISTIDQECVSFETFGADIDESFWKET 223
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 212 LSMPLDGYDVS-----MERGDAFVAPPSAD-----DMDYVLGVFMESGEADL 254
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 224 LYSODEHNVNSDLEVAGLVEIQOEFONLGSANNEMIFDSEMDFWFDVLAARTGGEDL 281
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

RESULT 13
 ADN72611 standard; protein; 285 AA.

```

XX ADN72611;
XX
XX 15-JUL-2004 (first entry)
XX
XX Thale cress protein upregulated in E2Fa/Dpa expressing plants Segid 506.
XX
XX plant; transgenic; E2Fa/Dpa transcription factor; growth regulator;
XX animal feed product; thale cress; cell wall biosynthesis;
XX nitrogen metabolism; carbon metabolism.
XX
XX Arabidopsis thaliana.
XX
XX WO2004035798-A2.
XX
XX 29-APR-2004.
XX
XX 20-OCT-2003; 2003WO-EP011658.
XX
XX 18-OCT-2002; 2002EP-00079408.
XX

```

PA (CROP-) CROPEDESIGN NV.
 XX Inze D, De Veylder L, Vlieghe K;
 PT WPI; 2004-348466/32.
 DR N-PSDB; ADN72610.
 XX

PT Altering plant characteristic, useful for producing plants for enzyme or
 PT pharmaceutical production comprises modifying in a plant, expression of
 PT one or more nucleic acids and/or modifying level or activity of one or
 PT more proteins.

Claim 1; SEQ ID NO 506; 134bp; English.

XX This invention relates to a novel method for altering one or more plant
 CC characteristics. Specifically, it refers to identifying genes that are up
 CC - or down-regulated in transgenic plants overexpressing the heterodimeric
 CC E2Fa/Dpa transcription factor of Arabidopsis and using these sequences to
 CC alter plant characteristics accordingly. The present invention describes
 CC generating transgenic plants for the production of growth regulators,
 CC enzymes, therapeutics, pharmaceuticals and animal feed products, where
 CC the altered plant characteristics are selected from increased yield or
 CC biomass, enhanced survival capacity, stress tolerance, plant architecture
 CC or physiology, altered endoreduplication, biochemistry, signal
 CC transduction, storage lipid mobilization and/or altered photosynthesis,
 CC each relative to the corresponding wild type plants. Accordingly, these
 CC sequences can also be useful as positive or negative selectable markers
 CC during transformation of cells or tissues. The identified genes play a
 CC role in a variety of biological processes such as DNA replication, cell
 CC wall biosynthesis, nitrogen and/or carbon metabolism or they function as
 CC transcription factors. This polypeptide sequence is thale cress protein
 CC expressed by a gene upregulated 1.3 fold or more in plants overexpressing
 CC the E2Fa/Dpa transcription factor, given in an exemplification of the
 CC invention.

XX Sequence 285 AA;

Query Match 48.4%; Score 661.5; DB 8; Length 285;
 Best Local Similarity 49.0%; Pred. No. 3.2e-55;
 Matches 146; Conservative 25; Mismatches 66; Indels 61; Gaps 6;

```

OY 1 MGRAPCCCKMGLKKGPMTPBEDKVLVAH1QRHGNWRALPRQAGILRCGKSCRLRWNY 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 MGRAPCCCKMGLKKGPMTPBEDQILVSFLNHGSHWRALPRQAGILRCGKSCRLRWNY 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 61 LRPDIKRGNFSEEDTTIHLHELGNRWSAIAALPRTDNEIKVWHTHLKKRLDAPA 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 LRPDIKRGNFTEEBDAIISLHQILGNRWSAIAAKLPRTDNEIKVWHTHLKKRLE-DY 119
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 121 OCGHVAASGGKHKPKSAKKPAAAAAAPSPERSASSVTESSWASSVAEHNAGIS 180
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 120 QPAKPKTSNKKKGTTPKS-----ESVITSSNSTRESSELAIS---SNPSGES 163
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 181 SASASVCAKESSFTSASEE-----FOIDSPWSET 211
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 164 LFTSPSTSEVSMTLISHDGYSEINMNDKPGDISTIDQECVSFETFGADIDESFWKET 223
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 212 LSMPLDGYDVS-----MERGDAFVAPPSAD-----DMDYVLGVFMESGEADL 254
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 224 LYSODEHNVNSDLEVAGLVEIQOEFONLGSANNEMIFDSEMDFWFDVLAARTGGEDL 281
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```

RESULT 14
 ADX91441 standard; protein; 304 AA.

```

XX ADX91441;
XX
XX 21-APR-2005 (first entry)
XX
XX Plant full length insert polypeptide segid 54105.
XX
XX plant protectant; plant growth regulant; gene therapy; plant;
XX

```

KW recombinant DNA construct; physical array; plant breeding marker;
 KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
 KW extreme osmotic condition; pathogen tolerance; pest tolerance;
 KW growth rate; cell cycle pathway; disease resistance;
 KW galactomannan production; lignin production; plant growth regulator;
 KW yield; plant growth; plant development; seed oil; protein yield;
 KW protein content.
 OS Unidentified.
 XX
 XX US2004034888-A1.
 XX
 XX PD 19-FEB-2004.
 XX
 XX PF 28-APR-2003; 2003US-00425114.
 XX
 XX PR 06-MAY-1999; 99US-00304517.
 XX PR 05-NOV-2001; 2001US-00985678.
 XX
 XX PA (LITU/) LIU J.
 XX PA (ZHOU/) ZHOU Y.
 XX PA (KOVA/) KOVALIC D. K.
 XX PA (SCRE/) SCREEN S. E.
 XX PA (TABAS/) TABASKA J. E.
 XX PA (CAOY/) CAO Y.
 XX
 XX PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y,
 XX
 XX DR WPI; 2004-180133/17.
 XX
 XX PT New recombinant DNA construct, useful for improving plant tolerance to
 PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
 PT pests, for conferring increased resistance to plant disease, or for
 PT improving yield.
 XX
 XX PS Claim 1, SEQ ID NO 54105; 15pp; English.
 XX
 CC The invention describes a recombinant DNA construct comprising a
 CC polynucleotide consisting of a sequence encoding an amino acid sequence
 CC available in electronic form from the US patent office at
 CC ftp.segdata.uspto.gov/sequence.html?docid:2004034888. The polynucleotide
 CC of the invention are also useful in physical arrays of molecules and as
 CC plant breeding markers. The recombinant DNA construct is useful for
 CC improving plant tolerance to cold, heat, drought, herbicides, extreme
 CC osmotic conditions, pathogens or pests, for manipulating growth rate in
 CC plant cells by modification of the cell cycle pathway, for conferring
 CC increased resistance to plant disease, for producing galactomannan,
 CC lignin or plant growth regulators, for increasing the rate of homologous
 CC recombination in plants, for improving yield by modification of
 CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
 CC or by providing improved plant growth and development under at least one
 CC stress condition or for modifying seed oil or protein yield and/or
 CC content. This is the amino acid sequence of a plant full length insert
 CC polypeptide that can be used in the recombinant DNA construct of the
 CC invention.
 XX
 XX SQ Sequence 304 AA;
 XX
 Query Match 48.4%; Score 661.5; DB 8; Length 304;
 Best Local Similarity 49.0%; Pred. No. 3.6e-55;
 Matches 146; Conservative 25; Mismatches 66; Indels 61; Gaps 6;
 QY 1 MGRAPCCCKGKGLKGGWTBBDVLYAHIORHGWRRALPKAGILRGCKSRLWVNY 60
 DB 20 MGRAPCCCKGKGLKGGWTBBDVLYAHIORHGWRRALPKAGILRGCKSRLWVNY 79
 QY 61 LRPDIRGNFTKEEDPAIISLHOLGNRSALAAKIPGRDNEIKVMHTLKKRLDAPA 120
 DB 80 LRPDIRGNFTKEEDPAIISLHOLGNRSALAAKIPGRDNEIKVMHTLKKRLDAPA 138
 QY 121 OGSHVAVSGGKKHKKPKSAKKPAAAAAPPASPERSASSVTSSMASSVAEEHGNAGIS 180
 DB 139 QPAKPTSNKKKOTKPKS-----ESVITSSNTRSESLADS-----SNPSGES 182

QY 181 SASASVCAKESSFTSASE-----FOIDSPKSET 211
 DB 183 LFTSPSTSESVSMPLTISHDGSNEINMDNKPQDISTIDQCVSFETFGADIDBSFKET 242
 QY 212 LSMPLDGYDVS-----MEPGDAFVAPPSAD-----DMDYWLGVFMESGEAODL 254
 DB 243 LYSQDEHNVNSDLEFVAGLVEIQGFQNGSNANMENIFDSEMDFWFDVLAFTGEGDL 300
 RESULT 15
 ADX71586
 ID ADX71586 standard; protein; 313 AA.
 XX
 XX AC ADX71586;
 XX
 XX DT 21-APR-2005 (first entry)
 XX
 XX DE Plant full length insert polypeptide seqid 40952.
 KW plant protectant; plant growth regulant; gene therapy; plant;
 KW recombinant DNA construct; physical array; plant breeding marker;
 KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
 KW extreme osmotic condition; pathogen tolerance; pest tolerance;
 KW growth rate; cell cycle pathway; disease resistance;
 KW galactomannan production; lignin production; plant growth regulator;
 KW yield; plant growth; plant development; seed oil; protein yield;
 KW protein content.
 OS Unidentified.
 XX
 XX OS
 XX PN US2004034888-A1.
 XX
 XX PD 19-FEB-2004.
 XX
 XX PF 28-APR-2003; 2003US-00425114.
 XX
 XX PR 06-MAY-1999; 99US-00304517.
 XX PR 05-NOV-2001; 2001US-00985678.
 XX
 XX PA (LITU/) LIU J.
 XX PA (ZHOU/) ZHOU Y.
 XX PA (KOVA/) KOVALIC D. K.
 XX PA (SCRE/) SCREEN S. E.
 XX PA (TABAS/) TABASKA J. E.
 XX PA (CAOY/) CAO Y.
 XX
 XX PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y,
 XX
 XX DR WPI; 2004-180133/17.
 XX
 XX PT New recombinant DNA construct, useful for improving plant tolerance to
 PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
 PT pests, for conferring increased resistance to plant disease, or for
 PT improving yield.
 XX
 XX PS Claim 1, SEQ ID NO 40952; 15pp; English.
 XX
 CC The invention describes a recombinant DNA construct comprising a
 CC polynucleotide consisting of a sequence encoding an amino acid sequence
 CC available in electronic form from the US patent office at
 CC ftp.segdata.uspto.gov/sequence.html?docid:2004034888. The polynucleotide
 CC of the invention are also useful in physical arrays of molecules and as
 CC plant breeding markers. The recombinant DNA construct is useful for
 CC improving plant tolerance to cold, heat, drought, herbicides, extreme
 CC osmotic conditions, pathogens or pests, for manipulating growth rate in
 CC plant cells by modification of the cell cycle pathway, for conferring
 CC increased resistance to plant disease, for producing galactomannan,
 CC lignin or plant growth regulators, for increasing the rate of homologous
 CC recombination in plants, for improving yield by modification of
 CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
 CC or by providing improved plant growth and development under at least one
 CC stress condition or for modifying seed oil or protein yield and/or

CC content. This is the amino acid sequence of a plant full length insert
CC polypeptide that can be used in the recombinant DNA construct of the
CC invention.

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 23, 2006, 23:59:07 ; Search time 41 Seconds
(without alignments)
603.115 Million cell updates/sec

Title: US-10-521-811-2

Perfect score: 1368
Sequence: 1 MGRAPCCCKMKGLKGPWTPB.....MDYVLGVFMESGEADLPQI 257

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : PIR 80: *
1: p1r1: *
2: p1r2: *
3: p1r3: *
4: p1r4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1368	100.0	257	2	T03825	myb protein homolo
2	835.5	61.1	288	2	T05954	transcription fact
3	709.5	51.9	280	1	S26604	myb-related protei
4	697.5	51.0	276	2	T03823	probable myb-relat
5	687	50.2	265	2	T07395	myb-related transc
6	669.5	48.9	278	2	T03850	myb-related protei
7	628.5	45.9	246	2	D86197	hypothetical prote
8	623.5	45.6	246	1	S71283	myb-related protei
9	608	44.4	249	2	E84717	probable MYB fam1
10	582	42.5	122	1	S58294	myb-related protei
11	563.5	41.2	340	1	S04898	myb-related protei
12	562	41.1	274	2	D86300	hypothetical prote
13	550	40.2	368	2	T03828	myb protein - rice
14	546	39.9	299	2	T47917	probable transcrip
15	532	38.9	325	2	T51509	probable transcrip
16	529	38.7	296	2	A96603	probable myb-fam1
17	527	38.5	376	2	T03988	myb-like transcrip
18	525.5	38.4	421	1	S26605	myb-related protei
19	524.5	38.3	399	1	A39697	maize myb-related
20	517	37.8	326	2	T49966	myb-related protei
21	516.5	37.8	321	1	S45338	myb-related protei
22	513.5	37.5	323	2	T51621	myb-like protein f
23	512.5	37.5	324	2	B85064	MYB-like protein f
24	511.5	37.4	323	2	T51645	myb-related transc
25	509.5	37.2	239	2	T02984	myb-related protei
26	508.5	37.2	421	1	S24244	myb-related protei
27	508	37.1	365	2	D86470	F21H2.9 protein -
28	507.5	37.1	311	2	T03827	myb protein homolo
29	507.5	37.1	330	2	F96775	hypothetical prote

30	506.5	37.0	327	2	T01038	myb-related protei
31	505.5	37.0	282	2	B85327	probable transcrip
32	505.5	37.0	332	1	S58283	myb-related protei
33	505	36.9	343	2	T48050	probable transcrip
34	505	36.9	352	1	S58293	myb-related protei
35	500	36.5	453	2	T09745	myb-related protei
36	499.5	36.5	316	1	J00956	myb-related protei
37	498	36.4	276	2	T02985	myb-related protei
38	497	36.3	294	2	T09879	myb-related protei
39	495.5	36.2	282	2	T05690	myb-related transc
40	495.5	36.2	333	2	T45720	probable transcrip
41	494.5	36.1	282	2	T51632	myb-related transc
42	493.5	36.1	251	1	S35729	myb-related protei
43	490	35.8	274	1	J00957	myb-related protei
44	489.5	35.8	255	1	S04899	myb-related protei
45	489	35.7	347	2	T07398	myb-related transc

ALIGNMENTS

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RESULT 1
T03825
myb protein homolog - rice
C/Species: Oryza sativa (rice)
C/Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 31-Dec-2004
C/Accession: T03825
R/Coraggio, I.
submitted to the EMBL Data Library, February 1997
A/Reference number: Z15103
A/Accession: T03825
A/Status: preliminary; translated from GB/EMBL/DDBA
A/Molecule type: mRNA
A/Residues: 1-257 <COR>
A/Cross-references: UNIPROT:O04140; UNIPARC:UP100000ACEBA; EMBL.Y11414; PIDN:CAA72217.1
C/Experimental source: cv. Arborio, coleoptile
C/Genetics:
A/Gene: myb
C/Superfamily: Myb-related transcription activator; myb DNA-binding repeat homology
F/9-61/Domain: myb DNA-binding repeat homology <MYB1>
F/62-112/Domain: myb DNA-binding repeat homology <MYB>

Query Match      100.0%: Score 1368; DB 2; Length 257;
Best Local Similarity 100.0%: Pred No. 2.5e-94;
Matches 257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MGRAPCCCKMKGLKGPWTPBEDKVLVAHIQRHGHGWRALPKQAGLLRCGSKRLRWINY 60
      |||
Db      1 MGRAPCCCKMKGLKGPWTPBEDKVLVAHIQRHGHGWRALPKQAGLLRCGSKRLRWINY 60

QY      61 LRPDIKRGNFSKEEDTTIHLHELGNRWSAIAARLPGRTDNEIKVWMTHLKKRLDAPA 120
      |||
Db      61 LRPDIKRGNFSKEEDTTIHLHELGNRWSAIAARLPGRTDNEIKVWMTHLKKRLDAPA 120

QY      121 QGSHVAASGCKKKKKPKSAKPPAAAAAPASPERSASSSVTSSMASSVAEEHGNAGIS 180
      |||
Db      121 QGSHVAASGCKKKKKPKSAKPPAAAAAPASPERSASSSVTSSMASSVAEEHGNAGIS 180

QY      181 SASASVCAKEESSFTSASEFOIDSFWSETLSMPLDGYVSNPEPDAFVAPPADMDY 240
      |||
Db      181 SASASVCAKEESSFTSASEFOIDSFWSETLSMPLDGYVSNPEPDAFVAPPADMDY 240

QY      241 WLGVFMESGEADLPQI 257
      |||
Db      241 WLGVFMESGEADLPQI 257

RESULT 2
transcription factor myb4 - barley (fragment)
C/Species: Hordeum vulgare (barley)
C/Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 31-Dec-2004
C/Accession: T05954
```


A:Cross-references: UNIPROT:Q04174; UNIPARC:UPI00000A561B; EMBL:X98308; NID:g1370139; P
 A:Experimental source: cultivar Ailes Craig; hypocotyl
 C:Genetics:
 A:Gene: THM18
 C:Superfamily: Myb-related transcription activator; myb DNA-binding repeat homology
 C:Keywords: DNA binding; transcription regulation
 F:9-61/Domain: myb DNA-binding repeat homology <MYB1>
 F:62-112/Domain: myb DNA-binding repeat homology <MYB>

Query Match 50.2%; Score 687; DB 2; Length 265;
 Best Local Similarity 50.7%; Pred. No. 8.1e-44;
 Matches 143; Conservative 38; Mismatches 57; Indels 44; Gaps 9;

QY 1 MGRAPCCCKMGLKGGWTPEDDKVLAHIOHGHGWRALPKOAGLLRCGSKRLRWNY 60
 DB 1 MGRAPCCCKMGLKGGWTPEDDKVLAHIOHGHGWRALPKOAGLLRCGSKRLRWNY 60
 QY 61 LRPDIKRGNFKEEBEDTIIHLHLLGNRWSAIAARLPGRDNEIKVWHTLKKRLDAPA 120
 DB 61 LRPDIKRGNFKEEBEDTIIHLHLLGNRWSAIAARLPGRDNEIKVWHTLKKRLDAPA 117
 QY 121 OGCHVAASGKGGKHKKK--SAKKPAAAAA-----PPASPERASSSVTE 163
 DB 118 --NYPCQNSKRSKTSKSHVSNKGPRTSESNNSDLSTKQAIKIPNSPOLSSS---E 171
 QY 164 SSMASVAEHEHGNAGISSASVCAKEESSFTSSEF-QIDSPFMSSETLSMP---LDGY 219
 DB 172 MSSVTILVDD-----NQWYIKEBKTESSSSSEYFKIDSPFADELSTENNMITGH 222

QY 220 D-----VSMERGDAP-VAPPSADMDMYLGVFMESGEAODLPQ 256
 DB 223 DGEIGVEENVDIFTTSSKMEEDMDPMYVFIKTGDLPELPE 264

RESULT 6
 T03850
 myb-related protein myb1, TMV-inducible - common tobacco
 C:Species: Nicotiana tabacum (common tobacco)
 C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 31-Dec-2004
 C:Accession: T03850
 R:Yang, Y.; Kleesig, D.F.
 Proc. Natl. Acad. Sci. U.S.A. 93, 14972-14977, 1996
 A:Title: Isolation and characterization of a tobacco mosaic virus-inducible myb oncogene
 A:Reference number: Z15119; MUID:97121500; PMID:8962166
 A:Accession: T03850
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-278 <YAN>
 A:Cross-references: UNIPROT:P93391; UNIPARC:UPI000009F9F2; EMBL:U72762; NID:g1732246; P
 A:Experimental source: strain Xanthi nc
 C:Genetics:
 A:Gene: myb1
 C:Superfamily: Myb-related transcription activator; myb DNA-binding repeat homology
 C:Keywords: DNA binding; transcription regulation
 F:9-61/Domain: myb DNA-binding repeat homology <MYB1>
 F:62-112/Domain: myb DNA-binding repeat homology <MYB>

Query Match 48.9%; Score 669.5; DB 2; Length 278;
 Best Local Similarity 47.2%; Pred. No. 1.7e-42;
 Matches 141; Conservative 37; Mismatches 56; Indels 65; Gaps 10;

QY 1 MGRAPCCCKMGLKGGWTPEDDKVLAHIOHGHGWRALPKOAGLLRCGSKRLRWNY 60
 DB 1 MGRAPCCCKMGLKGGWTPEDDKVLAHIOHGHGWRALPKOAGLLRCGSKRLRWNY 60
 QY 61 LRPDIKRGNFKEEBEDTIIHLHLLGNRWSAIAARLPGRDNEIKVWHTLKKRLDAPA 118
 DB 61 LRPDIKRGNFKEEBEDTIIHLHLLGNRWSAIAARLPGRDNEIKVWHTLKKRLDAPA 120
 QY 119 PAOGCHVAASGKGGKHKKK--AKKPAAAAA-----APPASPERASSS 160
 DB 121 PQO-----NSKRHSKSNHDSKGPJTSSSNNSDLTIINTOKHIDSPVLAENSPQISS 173

QY 161 VTSSMASVAEHEHGNAGISSASVCAKEESSFTSSEF-QIDSPFMSSETLS----- 213
 DB 174 STEMSTVTLV-DH-----QMVIYKOE--VMESSEYFPRIDESFWDELDTDNMS 221

QY 214 -----MPLDGYVSMERGDAPVAPPSADMDMYLGVFMESGEAODLPQ 256
 DB 222 STDHVVAAANQELQVQLPFSSF---KEENVDIATKMEEDMDPMYVFIKTGDLPELPE 277

RESULT 7
 D86197
 hypothetical protein [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2004
 C:Accession: D86197
 R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso
 Chin, C.W.; Chung, M.K.; Com, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.
 Nature 408, 816-820, 2000
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luo, J.S.; Malt, R.; Marziani
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shim, P.; Southwick, A.M.; Sun, H.; Tallon,
 Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A:Reference number: A86141; MUID:21016719; PMID:11130712
 A:Accession: D86197
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-246 <STO>
 A:Cross-references: UNIPROT:Q91LNC9; UNIPARC:UPI00000A8D57; GB:AE005172; NID:g8844123; P
 C:Genetics:
 A:Map position: 1
 C:Superfamily: Myb-related transcription activator; myb DNA-binding repeat homology

Query Match 45.9%; Score 628.5; DB 2; Length 246;
 Best Local Similarity 48.0%; Pred. No. 1.6e-39;
 Matches 132; Conservative 35; Mismatches 59; Indels 49; Gaps 8;

QY 1 MGRAPCCCKMGLKGGWTPEDDKVLAHIOHGHGWRALPKOAGLLRCGSKRLRWNY 60
 DB 1 MGRAPCCCKMGLKGGWTPEDDKVLAHIOHGHGWRALPKOAGLLRCGSKRLRWNY 60
 QY 61 LRPDIKRGNFKEEBEDTIIHLHLLGNRWSAIAARLPGRDNEIKVWHTLKKRLDAPA 120
 DB 61 LRPDIKRGNFKEEBEDTIIHLHLLGNRWSAIAARLPGRDNEIKVWHTLKKRLDAPA 116
 QY 121 OGCHVAASGKGGKHKKKAKKP--AAAAAPASPERASSSVTSSMASVAEHEGNAG 178
 DB 117 -----HSGQNNKEDPVSTTAEMPTSPQOQSSSAD-----ISAITLGNND 161
 QY 179 ISSASVCAKEESSFTSASEFO-IDSPFMSSETLSMPD-----GYDVSMER 225
 DB 162 ISNSN-----KDSATSSSEDEVLAIIIDSEFWSFVLMDCDISGENEKKIEWEGSLDR 214
 QY 226 GDAFVAPPSADMDMYLGVFMS-----GEAODLPQ 256
 DB 215 ND-----KGYNHDMFHFHLLTSSCTIGENSDISE 245

RESULT 8
 S71283
 myb-related protein, 28K, leaf-specific - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 28-Oct-1996 #sequence_revision 27-Feb-1997 #text_change 31-Dec-2004
 C:Accession: S71283
 R:Kirik, V.; Koelle, K.; Misera, S.; Baumlein, H.
 A:Description: The expression of a new leaf-specific myb gene is shifted to late embryo
 A:Reference number: S71283
 A:Accession: S71283
 A:Molecule type: DNA
 A:Residues: 1-246 <KIR>

A:Cross-references: UNIPROT:Q39153; UNIPARC:UPI00000A0F29; EMBL:Z50869; NID:G1263092; PI
A:Experimental source: strain Columbia
C:Genetics:
A:Introns: 45/1; 88/2
C:Superfamily: Myb-related transcription activator; myb DNA-binding repeat homology
C:Keywords: DNA binding; duplication; nucleus; transcription regulation
F:9-61/Domain: myb DNA-binding repeat homology <MYB1>
F:62-112/Domain: myb DNA-binding repeat homology <MYB2>

Query Match 45.6%; Score 623.5; DB 1; Length 246;
Best Local Similarity 47.3%; Pred. No. 3.8e-39;
Matches 130; Conservative 37; Mismatches 59; Indels 49; Gaps 8;

QY 1 MGRAPCCCKMGLKKGPWTEEDKVLVAHIQRHGHGWRALPKQAGLLRCGSKRLRWNY 60
DB 1 MGRAPCCCKMGLKKGPWTEEDKVLVAHIQRHGHGWRALPKQAGLLRCGSKRLRWNY 60
QY 61 LRPDIKRGNFSEEDTIIHLHLLGNRWSAIAARLPGRTDNEIKVWHTHLKKRLDAPA 120
DB 61 LRPDIKRGNFSEEDTIIHLHLLGNRWSAIAARLPGRTDNEIKVWHTHLKKRLDAPA 120
QY 121 OGCHVAASGKKHKKPKSAKKP-AAAAAPASPERSASSSVTSSMASSVAEEHGNAG 178
DB 61 LRPDIKRGNFSEEDTIIHLHLLGNRWSAIAARLPGRTDNEIKVWHTHLKKRLDAPA 116
QY 117 -----HHSQDNKKEDFVSTTAEMFPTSPOQSSSSAD-----ISAITTGGNNND 161
DB -----HHSQDNKKEDFVSTTAEMFPTSPOQSSSSAD-----ISAITTGGNNND 161
QY 179 ISSASAVCAKEESSFTSASEFQ-IDDSFWSETL-----SMPDGYDVSMP 225
DB 162 INSN-----KDSATSSSEDLAIIIDSFSEVLTDCDISGNEKEKKEITWBSGLDR 214
QY 226 GDAFVAPSPADMDVYLGVFMS-----GEADLPQ 256
DB 215 ND-----KGYNDMEFWFHLTSSSCITGMSDISE 245

RESULT 9

probable MYB family transcription factor [imported] - Arabidopsis thaliana
E84717
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 31-Dec-2004
C:Accession: E84717
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: E84717
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-249 <STO>
A:Cross-references: UNIPROT:Q9SJX8; UNIPARC:UPI00000A5AFA; GB:A6002093; NID:G4432813; PI
A:Genetics:
A:Gene: Atg31180
A:Map position: 2
C:Superfamily: Myb-related transcription activator; myb DNA-binding repeat homology

Query Match 44.4%; Score 608; DB 2; Length 249;
Best Local Similarity 43.3%; Pred. No. 5.4e-38;
Matches 122; Conservative 38; Mismatches 62; Indels 60; Gaps 5;

QY 1 MGRAPCCCKMGLKKGPWTEEDKVLVAHIQRHGHGWRALPKQAGLLRCGSKRLRWNY 60
DB 1 MGRAPCCCKMGLKKGPWTEEDKVLVAHIQRHGHGWRALPKQAGLLRCGSKRLRWNY 60
QY 61 LRPDIKRGNFSEEDTIIHLHLLGNRWSAIAARLPGRTDNEIKVWHTHLKKRLDAPA 120
DB 61 LRPDIKRGNFSEEDTIIHLHLLGNRWSAIAARLPGRTDNEIKVWHTHLKKRLDAPA 120
QY 121 OGCHVAASGKKHKKPKSAKKPAAAAAPASPERSASSSVTSSMASSVAEEHGNAGS 180
DB 121 NNNG-----GDKVDVNGINETTNETTNGKSVYD 146
QY 181 SASASVCAKEESSFTSASEFQ-----IDDSFWSETLSMP-LDGYDVSMPGDA 228

DB 147 TASLQGFNSITTFPIISNDKODIMSYEDISALIDSFSDVISTVNSKNEKTIEDWEG 206
QY 229 EVAPPSA-----DDNDYLVGVFMS-----GEADLPQ 256
DB 207 LIDRNSKCKSYNSKLYNDMDMEFVFTSNRIEFSIDPE 248

RESULT 10

S58294
myb-related protein y19 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 14-Jan-1996 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004
C:Accession: S58294
R:Quaedvlieg, N.E.M.; Dockx, J.; Keultjes, G.G.M.; Sneekens, J.C.M.
submitted to the EMBL Data Library, July 1995
A:Reference number: S58294
A:Accession: S58280
A:Molecule type: DNA
A:Residues: 1-132 <QUA>
A:Cross-references: UNIPROT:Q39260; UNIPARC:UPI000009FC92; EMBL:X90384; NID:G928966; PI
C:Genetics:
A:Introns: 44/3; 88/3
C:Superfamily: Arabidopsis myb-related protein y19; myb DNA-binding repeat homology
C:Keywords: DNA binding; duplication; nucleus; transcription regulation
F:9-61/Domain: myb DNA-binding repeat homology <MYB1>
F:62-112/Domain: myb DNA-binding repeat homology <MYB2>

Query Match 42.5%; Score 582; DB 1; Length 122;
Best Local Similarity 85.5%; Pred. No. 2e-36;
Matches 100; Conservative 11; Mismatches 6; Indels 0; Gaps 0;

QY 1 MGRAPCCCKMGLKKGPWTEEDKVLVAHIQRHGHGWRALPKQAGLLRCGSKRLRWNY 60
DB 1 MGRAPCCCKMGLKKGPWTEEDKVLVAHIQRHGHGWRALPKQAGLLRCGSKRLRWNY 60
QY 61 LRPDIKRGNFSEEDTIIHLHLLGNRWSAIAARLPGRTDNEIKVWHTHLKKRLD 117
DB 61 LRPDIKRGNFSEEDTIIHLHLLGNRWSAIAARLPGRTDNEIKVWHTHLKKRLD 117

RESULT 11

S04898
myb-related protein 1 - maize
N:Alternate names: myb-related protein Zml
C:Species: Zea mays (maize)
C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 31-Dec-2004
C:Accession: S04898
R:Marocco, A.; Wiesenbach, M.; Becker, D.; Paz-Ares, J.; Saedler, H.; Salamini, F.; Roh
Mol. Gen. Genet. 216, 183-187, 1989
A:Title: Multiple genes are transcribed in Hordeum vulgare and Zea mays that carry the
A:Reference number: S04896; MUID:89313655; PMID:2664447
A:Accession: S04898
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-340 <MAR>
A:Cross-references: UNIPROT:P20024; UNIPARC:UPI000012FAD8
C:Superfamily: Myb-related transcription activator; myb DNA-binding repeat homology
C:Keywords: DNA binding; duplication; nucleus; transcription regulation
F:11-63/Domain: myb DNA-binding repeat homology <MYB1>
F:64-114/Domain: myb DNA-binding repeat homology <MYB2>

Query Match 41.2%; Score 563.5; DB 1; Length 340;
Best Local Similarity 49.4%; Pred. No. 1.6e-34;
Matches 118; Conservative 26; Mismatches 50; Indels 45; Gaps 6;

QY 2 GRAPCCCKMGLKKGPWTEEDKVLVAHIQRHGHGWRALPKQAGLLRCGSKRLRWNY 61
DB 4 GRAPCCAKYGLRGSWTPEEDKRLVAYIQHGHTRALPKQAGLLRCGSKRLRWNY 63
QY 62 RPDIKRGNFSEEDTIIHLHLLGNRWSAIAARLPGRTDNEIKVWHTHLKKRLDAPA 121
DB 64 RPDIKRGNFSEEDTIIHLHLLGNRWSAIAARLPGRTDNEIKVWHTHLKKRV----- 118

QY 122 GGHVAASGGKKKKPKSAKKPAAAAAPASPERASSSVT--ESSMASSVAEHNAGI 179
Db 119 -----AQREKKKAAGSGDAGTAPATAPLSSATSTTTNNSSGSGSGGQCTSRRE 168
QY 180 SASASVCACESSFTFSASEEFOIDDSFMSSETLMPDGYDVMEGDAFVAPPASDDM 238
Db 169 PRAT-DVC-----TLQPEDMDVSD-----MLVDG-----APPAQPM 199

RESULT 12

D86300

hypothetical protein F309.29[imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #ext_change 31-Dec-2004

C:Accession: D86300

R:Thelodis, A.; Ecker, J.R.; Palm, C.J.; Federpiet, N.A.; Kaul, S.; White, O.; Alonso,

Chen, N.F.; Hughes, B.; Hulzar, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopeon, C.; Khan, S.; Khaykin, E.; Kim, C.

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shim, P.; Southwick, A.M.; Sun, H.; Tallon,

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; M01D:21016719; PMID:11130712

A:Accession: D86300

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-274 <STO>

A:Cross-references: UNIPROT:Q9SA47; UNIPARC:UP1000009D685; GB:AE005172; NID:94966369; PI

C:Genetics:

A:Map position: 1

C:Superfamily: Myb-related transcription activator; myb DNA-binding repeat homology

Query Match 41.1%; Score 562; DB 2; Length 274;

Best Local Similarity 45.4%; Pred. No. 1.6e-34;

Matches 114; Conservative 36; Mismatches 67; Indels 34; Gaps 6;

QY 2 GRAPCCCKMGLKGPWTPEEDKVLVAHIORHGNMRLPKOAGLRCGSKRLRWNY 61
Db 4 GRAPCCCKMGLKGPWTPEEDKVLVAHIORHGNMRLPKOAGLRCGSKRLRWNY 63
QY 62 RPDYKRGNSKEEDTIIHLHLLGNRSVAIARLPGRTDNEIKYVWHTLKKRLDPAQ 121
Db 64 RPDYKRGNSKEEDTIIHLHLLGNRSVAIARLPGRTDNEIKYVWHTLKKRLDPAQ 123
QY 122 -GGHVAASGGKKKKPKSAKKPAAAAAPASPERASSSVTSSMASSVAEHNAGIS 180
Db 124 LNADRGSGKSLNEENSOE-----SSPNAMSFRA-----GSNITSSKDDAQIS 167
QY 181 SASASVCACESSFTFSASEE-----FOIDDSFMSSETLMPDGYDVMEGDAFV 230
Db 168 QMFEHLTVSE--FTQMLEVDKPELLEMPFDLPDIWTF-----IDGSDSFGQFENRAL 220
QY 231 APPSADMDY 241
Db 221 QSESEDEVK 231

RESULT 13

T03828

myb protein - rice

C:Species: Oryza sativa (rice)

C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #ext_change 31-Dec-2004

C:Accession: T03828

R:Coraggio, I.

submitted to the EMBL Data Library, February 1997

A:Reference number: Z15103

A:Accession: T03828

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-368 <COR>
A:Cross-references: UNIPROT:O04141; UNIPARC:UP100000A0C830; EMBL:Y11415; P1DN:CAA72218.1
A:Experimental source: cv. Arporio, coleoptile
C:Genetics:
A:Gene: myb
C:Superfamily: Myb-related transcription activator; myb DNA-binding repeat homology
F:62-112/pomatin: myb DNA-binding repeat homology <MYB>

Query Match

40.2%; Score 550; DB 2; Length 368;

Best Local Similarity 41.0%; Pred. No. 1.7e-33;

Matches 129; Conservative 35; Mismatches 75; Indels 76; Gaps 10;

QY 1 MGRAPCCCKMGLKGPWTPEEDKVLVAHIORHGNMRLPKOAGLRCGSKRLRWNY 60
Db 1 MGRAPCCCKMGLKGPWTPEEDKVLVAHIORHGNMRLPKOAGLRCGSKRLRWNY 60
QY 61 LRPDYKRGNSKEEDTIIHLHLLGNRSVAIARLPGRTDNEIKYVWHTLKKRL 116
Db 61 LRPDYKRGNSKEEDTIIHLHLLGNRSVAIARLPGRTDNEIKYVWHTLKKRL 120
QY 117 -DAPACGHHVAASGGKKKKPK-----SAPKPAAPAAAPPASPE----- 154
Db 121 IDPVTFA-----PRDLIDLTLKPAAPAAAYPTQADLDLRLALEPLAGYP 167
QY 155 ---RSASS---SVTSSMASSVAEHNAGISSASASVCACESSFT-----SASE 199
Db 168 DLRLASALPLPAVTTGAAPAAABOAFPLPWLQAGHAGQQQVTPPPPPPPAAT 227
QY 200 EFOIDDSFMSSETLMPDGYDVMEGDAFVAP-----PSADD-MDY 241
Db 228 QFLQATRS-----TACHQMPGLVHASPQOALQAGQDHMAAATCRGAVGHPSPYDNQLDY 283
QY 242 LGVMESEGAQDLP 256
Db 284 PALMQWASDASNLQ 298

RESULT 14

T47917

probable transcription factor MYB17 - Arabidopsis thaliana

N:Alternate names: protein T20K12.150

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #ext_change 31-Dec-2004

C:Accession: T47917; T51638

R:De Haan, M.; Maize, A.C.; Griwell, L.A.; Mewes, H.W.; Lemcke, K.; Mayer, K.F.X.; Que

submitted to the Protein Sequence Database, January 2000

A:Reference number: Z24480

A:Accession: T47917

A:Molecule type: DNA

A:Residues: 1-299 <DEH>

A:Cross-references: UNIPROT:Q9M2D9; UNIPARC:UP100000A65F8; EMBL:AL137898

A:Experimental source: cultivar Columbia; BAC clone T20K12

R:Kranz, H.D.; Denekamp, M.; Greco, R.; Jin, H.; Kranz, H.D.; Denekamp, M.; Greco, R.;

Paz-Ares, J.; Welsch, B.

Plant J. 16, 263-276, 1998

A:Title: Towards functional characterisation of the members of the R2R3-MYB gene from A

A:Reference number: Z14349; M01D:9839469; PMID:9839469

A:Accession: T51638

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 76-116, 'Y', 118-299 <KRA>

A:Cross-references: UNIPARC:UP100000A0A888; EMBL:AF062866; P1DN:AA03508.1

A:Experimental source: cultivar Columbia

C:Genetics:

A:Gene: MYB17

A:Map position: 3

A:Introns: 45/1; 88/2

A:Note: T20K12.150

C:Superfamily: Myb-related transcription activator; myb DNA-binding repeat homology

Query Match 39.9%; Score 546; DB 2; Length 299;
Best Local Similarity 43.4%; Pred. No. 2.7e-33;
Matches 121; Conservative 35; Mismatches 81; Indels 42; Gaps 5;

```

QY      1 MGRAPCCCEKMGILKKGPWTEBEDKVLVAHIQRHGHGNWRALPKQAGLLRCGKSCRLRWINY 60
DB      1 MGRTPCCDIXIGLKKGPWTEBEDVLVAHIKKNGHGSWRTLPKLAGLLRCGKSCRLRWINY 60
QY      61 LRPDIKRGNFSKEEDPTIHLHELIGNRWSAIAARLPGRDNEIKVWHTHLKKRL---D 117
DB      61 LRPDIKRGPFTADEEKLVLQHLAILGNRAAIIAOLPGRDNEIKVWHTHLKKRLLSMG 120
QY      118 APAQGCHVAASGGKQKHKPKSAKPPAAAAAPPASPERSASSVTSSMASSVAEEHG-- 175
DB      121 LDPRTHEPLPSYGLAQAPSS---PTTRHMAQWESARVEAEARLSRESMLFSPSPYSGVV 177
QY      176 -----NAGISSASAVCAKESSFTSASEEFOI-----DDSFMSSETLS 213
DB      178 KTECHFLRIWNSSEIGEAFFNLAPLDESTITTSQSPCSRATSTSSALLKSTNSWGGEVY 237
QY      214 MPIDGYDVSMERPD-----AFVAPPSADMDY 240
DB      238 VAHGSDDYSPYGNLDEDDSTDSALQLLLDFPISDDMSF 276

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RESULT 15

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T51509
probable transcription factor (MYB9) - Arabidopsis thaliana
N:Alternate names: protein F5E19_110
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 31-Dec-2004
C:Accession: T51509
R:Sato, S.; Nakamura, Y.; Kaneko, T.; Kato, T.; Asamizu, E.; Kotani, H.; Tabata, S.; Mew
submitted to the Protein Sequence Database, August 2000
A:Reference number: Z25394
A:Accession: T51509
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-325 <SAT>
A:Cross-references: UNIPROT:Q9LFE1; UNIPARC:UP100000AA6D3; EMBL:AL391147
A:Experimental source: cultivar Columbia; BAC clone F5E19
C:Genetics:
A:Map position: 5
A:Introns: 88/2
A:Note: F5E19_110
C:Superfamily: Myb-related transcription activator; myb DNA-binding repeat homology

```

Query Match 38.9%; Score 532; DB 2; Length 325;

Best Local Similarity 44.3%; Pred. No. 3.2e-32; Matches 116; Conservative 32; Mismatches 66; Indels 48; Gaps 7;

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QY      1 MGRAPCCCEKMGILKKGPWTEBEDKVLVAHIQRHGHGNWRALPKQAGLLRCGKSCRLRWINY 60
DB      1 MGRSPCCDENGILKKGPWTEBEDKILDIHQHGHGSWRALPKQAGLNRCCSKSCLRWINY 60
QY      61 LRPDIKRGNFSKEEDPTIHLHELIGNRWSAIAARLPGRDNEIKVWHTHLKKRLDAPA 120
DB      61 LRPDIKRGNFTREEQTIINLHSLGNKMSIAGNLPGRDNEIKVWHTHLKKL---L 117
QY      121 QGCHVAASGGKQKHKPKS-----AKPPAAAAAPPAS----- 152
DB      118 QMGIDPVT-----HRPRTHLNVLALPOLIAANFNLSLINLNQNVOLDATTAKAQLH 172
QY      153 ---PERSASSVTSSMASSVAEEHGNAGISSASAVCAKESSFTSASEEFO---IDS 206
DB      173 TMIQVLTNNNTNTPSSSTMQNSNTNLFQAS---YIENQNLFGQSGNFSHILEDEN 228
QY      207 FMSSET--LSMPIDGYDVSMERPD 226
DB      229 LMVKTQIIDNPLDPSFSSPIQPG 250

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Search completed: June 24, 2006, 00:04:35
Job time : 42 secs

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: June 25, 2006, 08:01:37 ; Search time 46 Seconds
(without alignments)
6264.114 Million cell updates/sec

Title: US-10-521-811-1

Perfect score: 1202
Sequence: 1 cagcgcgcctccctcccaaga.....gctcaaaaaaaaaaaaaa 1202

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 296510 seqs, 119862409 residues

Total number of hits satisfying chosen parameters: 593020

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications NA New.*
1: /EMC_Celerra_SIDS3/Pctodata/1/pubpna/US09_NEW_PUB.seq.*
2: /EMC_Celerra_SIDS3/Pctodata/1/pubpna/US06_NEW_PUB.seq.*
3: /EMC_Celerra_SIDS3/Pctodata/1/pubpna/US07_NEW_PUB.seq.*
4: /EMC_Celerra_SIDS3/Pctodata/1/pubpna/US08_NEW_PUB.seq.*
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6: /EMC_Celerra_SIDS3/Pctodata/1/pubpna/US10_NEW_PUB.seq.*
7: /EMC_Celerra_SIDS3/Pctodata/1/pubpna/US11_NEW_PUB.seq.*
8: /EMC_Celerra_SIDS3/Pctodata/1/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	269.2	22.4	1326	US-10-449-902-11663	Sequence 11663, A
2	251.8	20.9	1399	US-10-449-902-11373	Sequence 11273, A
3	248.2	20.6	1163	US-10-449-902-10135	Sequence 10135, A
4	227.6	18.9	1027	US-10-449-902-5864	Sequence 5864, Ap
5	223.6	18.6	1139	US-10-449-902-8691	Sequence 8691, Ap
6	222.8	18.5	1284	US-10-953-349-33713	Sequence 33713, A
7	217.8	18.1	1389	US-10-449-902-7552	Sequence 7552, Ap
8	217.6	18.1	1037	US-10-449-902-2899	Sequence 2899, Ap
9	217.4	18.1	995	US-10-449-902-26232	Sequence 26232, A
10	217	18.1	1087	US-10-449-902-3902	Sequence 3902, Ap
11	212.4	17.7	1031	US-10-449-902-11361	Sequence 11361, A
12	209.8	17.5	1042	US-10-449-902-11212	Sequence 11212, Ap
13	209.8	17.5	1069	US-10-449-902-16336	Sequence 16336, A
14	208.2	17.3	1023	US-10-449-902-19393	Sequence 19393, A
15	203	16.9	1048	US-10-449-902-3635	Sequence 3635, Ap
16	203	16.9	1054	US-10-449-902-3280	Sequence 3280, Ap
17	202.6	16.9	1464	US-10-449-902-13496	Sequence 13496, A
18	193.6	16.1	1117	US-10-953-349-9698	Sequence 9698, Ap
19	189.8	15.8	1262	US-10-449-902-11177	Sequence 11177, A
20	187.8	15.6	1089	US-10-449-902-11704	Sequence 11704, A
21	187	15.6	1337	US-10-953-349-22500	Sequence 22500, A
22	180.8	15.0	1031	US-10-449-902-10911	Sequence 10911, A
23	176.8	14.7	1287	US-10-953-349-8308	Sequence 8308, Ap
24	175.8	14.6	1309	US-10-449-902-9787	Sequence 9787, Ap
25	175.2	14.6	2407	US-10-449-902-22163	Sequence 22163, A

26	173.8	14.5	2327	US-10-449-902-15504	Sequence 15504, A
27	173	14.4	1894	US-10-449-902-3075	Sequence 3075, Ap
28	173	14.4	2207	US-10-449-902-24194	Sequence 24194, A
29	169	14.1	2142	US-10-449-902-6303	Sequence 6303, Ap
30	162.6	13.5	2306	US-10-449-902-27399	Sequence 27399, A
31	162.6	13.5	2412	US-10-449-902-6813	Sequence 6813, Ap
32	158	12.9	1405	US-10-449-902-12272	Sequence 12272, A
33	154.8	12.9	1101	US-10-953-349-16710	Sequence 16710, A
34	153.6	12.8	1306	US-10-449-902-22352	Sequence 22352, A
35	148.6	12.4	1584	US-10-953-349-30202	Sequence 30202, A
36	147	12.2	1723	US-10-449-902-1432	Sequence 1432, Ap
37	142.2	11.8	1421	US-10-449-902-28013	Sequence 28013, A
38	142.2	11.8	1393	US-10-953-349-10214	Sequence 10214, A
39	138.4	11.5	1680	US-10-449-902-9371	Sequence 9371, Ap
40	136.2	11.3	777	US-11-179-064B-75	Sequence 75, Appl
41	135.4	11.3	1404	US-10-449-902-18697	Sequence 18697, A
42	132.2	11.0	1575	US-10-449-902-10076	Sequence 10076, A
43	126.2	10.5	936	US-10-953-349-5011	Sequence 5011, Ap
44	122.6	10.2	1019	US-10-953-349-25118	Sequence 25118, A
45	117.8	9.8	1426	US-10-953-349-24253	Sequence 24253, A

ALIGNMENTS

RESULT 1
US-10-449-902-11663
; Sequence 11663, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agricultural Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; TITLE OF INVENTION: FOUNDATION FOR ADVANCEMENT OF INTERNATIONAL SCIENCE.
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; PRIOR FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11663
; LENGTH: 1326
; TYPE: DNA
; ORGANISM: Oryza sativa
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AK109011
; DATABASE ENTRY DATE: 2002-08-28
US-10-449-902-11663

Query Match 22.4%; Score 269.2; DB 6; Length 1326;
Best local similarity 70.1%; Pred. No. 7.7e-51;
Matches 380; Conservative 0; Mismatches 153; Indels 9; Gaps 1;

QY	77	CAATGGGAGGAGCTCTGCTCGGAGAGATGGGCTCAAGAGGTCATGAGCCCGG	136
DB	251	CGATGGGAGGAGCGCGCTCGGAGAGAGAGGCTGAGAGAGGAGCGGAGCGCCG	310
QY	137	AGGAGGACAGGTCCTCGTGGCCATCCAGCCGACCGGACCGGCACTGGCGGCGC	196
DB	311	AGGAGGACAGCGCTCGTGGCTCATCTCGCGCCACCGGACCGGCACTGGCGGCGG	370
QY	197	TGCGGAGGAGCGGCTGCTGCTGGCGGAGAGCTGCCGAGTCCGATGATCACT	256
DB	371	TGCGGAGGAGCGGCTGCTGCTGGCGGAGAGCTGCGAGTCCGATGATCACT	430
QY	257	ACCTGGGAGGAGCATCAAGCGGCGCACTTCTCAAGAGGAGGAGGACCATCATTC	316
DB	431	ACCTGGGAGGAGCATCAAGCGGCGGCACTTCTCAAGAGGAGGAGGACCATCATTC	490

Qy	317	ATCTCCAGAGCTGCTTGCCCAAGGTGGTCCGCAATTGCCGACAGTTGCCCGGGAGGA	376
Db	491	GCCCTCCACACTCCCTCGGCAACAGGTGGTCAAGCACTGCGCCCAAGTGC CGGTGCGA	550
Qy	377	CGGACACAGATCAAGAACTGTGGCACCCACTCAAGAAAGCCCTCGATG-----	430
Db	551	CTGACACAGAGATCAAGAACTGTGGCACACTCACTTCAAGAAAGGCTGGACAGAAAC	610
Qy	431	---CGCCGAGCTCAGGGCGGTCACTGTGCGGCGAAGCGGCGGCAAGAACCAAGACCGA	487
Db	611	GGAGCTCGCGCCGCGCGGTGGGTGGCGCGCGCGCCGACATACGCGCAACAGCCCA	670
Qy	488	AGAGCGCGAAGAACCGACGCGCGCCGCGCGCGCGCGCGCGGTGCGCCCGAGCGGTCCG	547
Db	671	AGGCGGCAAAAGAGCCGCGCGCGCTCAACGCGAGGCGGACGCGGTCCGTACGCTGACCA	730
Qy	548	CCTCGTCTCGGTGACGAGTCTCTCGATTGGCTCTGTCGTTGGCGGAGAGACAGGCACCG	607
Db	731	CCAGTAGCGGCGGTGACGTGCTCCACGAGTACCGAGTGTGTCGCTGTGCGGCGCAGCGCG	790
Qy	608	CC 609	
Db	791	AC 792	

RESULT 2

US-10-449-902-11273
Sequence 11273, Application US/10449902
Publication No. US20060123505A1
GENERAL INFORMATION:
APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 11273
LENGTH: 1399
TYPE: DNA
ORGANISM: *Oryza sativa*
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AK108621
DATABASE ENTRY DATE: 2002-08-28
US-10-449-902-11273

Query Match

Query Match	20.9%;	Score 251.8;	DB 6;	Length 1399;
Best Local Similarity	60.0%;	Pred. No. 5.5e-47;		
Matches 446;	Conservative	0;	Mismatches 282;	Indels 15;
				Gaps 1

	62	104	122	164	182	224	242	284
Oy	GGAGAGAGCAAGCATATGGGAGGGCTCCGTCTGCGAGAGATGGGGCTCAAGAG	121						
Db	GTGGGGGAGACGGCGCCATATGGGGAGGGCGCGTGTTCGACAAAGAGGGGCTCAAGAG	163						
Oy	GTCATGAGACGCCGGAGAGAGACAGTCTCTGTCGCGCCACATCCAGCGCCACAGGCACG	181						
Db	GGCCCTGGAGACGGCGGAGAGAGAAAGTCTCTCTGCACTACATCCAGGCCAAGGCCACG	223						
Oy	GCAACTGGGCGCCCTGCCCAAGCAAGCCGGCGTGTGCTTCGGCCAGAGCTGCGCGC	241						
Db	GCAAGCTGGGCGCTCTCTCCCAAGCTGCAAGGGCTGAACCGGTGCGGAAGCTGCCGCGC	283						
Oy	TCCGGTGATCAACTACTTGGCGCGGACATCAAGCGGGGCAACTTCTCCAGAGAGAG	301						
Db	TGCGGTGGAGCAACTACTTCCGGCGGACATCAAGAGCGCGGGCCCTTTCACGCGAGAGAGC	343						

QY	302	GGGACCATCATCATCATCTCCACGAGCGCTGTGGAAACAGGTGTCTCCGAATTGCCGCCA	361
Db	344	AGAAATCATGTGTCCAGCTCCACGGGCATGTGTGGCAACAATGTGTCAATGATGGGGCG	403
QY	362	GATTGCCCGGAGAGGACGACAAACGATTCAGAACGTGTGGCACACCTTCAGAAAGC	421
Db	404	AGTGTCCCGGCGCGGACCCACAAACGAACTTCAGAACTATTGGAACACTCACTTCMAAAGC	463
QY	422	-----GCCTCGATGGCGCGGCTCAAGGGCGGTCATGTCGCGGCGAGCGCG	466
Db	464	AGCTGTCCCGGATGGGCTTCGACGATCCGGCCGCCCGGGCGGGGGCTGTCCGGCGG	523
QY	467	GCAAGAAACACAAAGAGCCGAAGACGCGGAGAACGACGCCCGCGCCGCGCCGCGC	526
Db	524	CGCGTCATGAGCGCAGTGGGAGAACCGCGCGCTGAGAGCCGAGGGCGCGCTCTCC	583
QY	527	CGGCGTCGCCCGGAGCGGTCCTCGTGTGTGGTGAACGAGTCCTGATGGCTTCGTGG	586
Db	584	TCTCTCTCTCGGCGCTCGGGGAGACGACGATCAACGCCCGGCACACCACTTCG	643
QY	587	TGGCGGAGAGACACGGCAACGCCGGGATCACTCGGCGCTCGCGTCCGTGTGCCAAG	646
Db	644	CCTGTCTCTCTCCACCAACCGGGGGCCGTCGCGCGCCCGCCGAGTCAACCGCGGAAG	703
QY	647	AGGAGAGTCTTCACTCTCGGCTTCGAGAGTTCCAGATTCGACGACACTTGTGGCG	706
Db	704	TGTTCTCTCGGCTCTCGAACTTCAGACTCGGGGATCTCTTCGCAAGTAAAGCTGTGTG	763
QY	707	AGACGCTTCGATGCCGCTGACGCGGTACGAGTGTCCAATGAGCCCGCGACGCTTCG	766
Db	764	CGGGCGGGTCTGTGTCTCCCTTCGCGGGGAGACGTCAACGAAGACGCTGTGAAGCAGAGG	823
QY	767	TGCGCGCCGATCCCGCGACGAC	789
Db	824	AGGAGGCGGCGCGCGCGGAC	846

RESULT 3

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US-10-449-902-10135
/ Sequence 10135, Application US/10449902
/ Publication No. US20060123505A1
/ GENERAL INFORMATION:
/ APPLICANT: National Institute of Agrobiological Sciences.
/ APPLICANT: Bio-oriented Technology Research Advancement Institution
/ APPLICANT: The Institute of Physical and Chemical Research.
/ APPLICANT: Foundation for Advancement of International Science.
/ TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
/ FILE REFERENCE: MOA-00205YI-US
/ CURRENT APPLICATION NUMBER: US/10/449,902
/ CURRENT FILING DATE: 2003-05-29
/ PRIOR APPLICATION NUMBER: JP 2002-203269
/ PRIOR FILING DATE: 2002-05-30
/ PRIOR APPLICATION NUMBER: JP 2002-383870
/ PRIOR FILING DATE: 2002-12-11
/ NUMBER OF SEQ ID NOS: 56791
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 10135
/ LENGTH: 1163
/ TYPE: DNA
/ ORGANISM: Oryza sativa
/ PUBLICATION INFORMATION:
/ DATABASE ACCESSION NUMBER: AK107463
/ DATABASE ENTRY DATE: 2002-08-28
US-10-449-902-10135

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Query Match

Query Match	Score	DB	Length
Best Local Similarity	20.6%	248.2	6
	62.0%	Pred. No. 3.2e-46	
		W. number 37	
		radol	12
			1

	Matches	416;	Conservative	0;	Mismatches	243;	Inserts	12;	Gaps	1
QY	79	ATGGGAGAGGCTCGTGTGCGAGAGATGGGCTCAAGAGGGTCCATGAGACGCCGAG	138							
Db	179	ATGGGAGAGCACCTCTGTCTGCGCAGAGGTGGGCTTGAGAGAGGGCCCTGTGACGCGCGAG	238							

139 GAGACAAAGATCTCTGCGCCATCAACGCGCAGGCACTGGCGGCTG 198
239 GAGGACCAAGATCTCTGCGCCATCAACGCGCAGGCACTGGCGGCTG 298
199 CCCAACCAAGCGGCTGCTGCTGCGGCAAGAGCTGCGGCTGCGGCTG 258
299 CCCAACCTGCGAGGCTGCTGAGGCGGGAAGAGCTGCGGCTGCGGCTG 358
259 CTGCGGCGGCACTCAAGCGGCGGCACTTCTCCAGAGAGAGAGACATCAT 318
359 CTGAGGCGGCACTCAAGAGAGGCGCTCTCTCCAGAGAGAGAGAGAGAG 418
319 CTCCAGAGCTGCTGAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 378
419 CTGAGAGCGGCACTGCGGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 478
379 GACCAAGAGATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 438
479 GACCAAGAGATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 536
439 CAGGCGGCTCATGTCGCGGCGAGCGGCGGCAAGAGAGAGAGAGAGAGAG 498
537 -----GCATCAACCCCGTCAACCAACAGCGCGCTGCTGCTGCTGCG 586
499 AAGCAGCG 558
587 CCGGAGAGAGATGCGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 646
559 GTGACGAGATCTCTGATGCGCTGCTGCGAGAGAGAGAGAGAGAGAGAG 618
647 GAG 706
619 TGGCGGCTGCGCGCTGCTGCTGCGCGCAAGAGAGAGAGAGAGAGAGAG 678
707 CCGGCG 766
679 TTCAGATGAG 738
767 TCCCGGCTGCTGCTGCTGCTGCGCGCTGCGCGCTGCGCGCTGCGCGAG 826
739 GTGCTCATGA 749
827 GAGCCCATGTA 837

RESULT 4
US-10-449-902-5864
; Sequence 5864, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agricultural Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USBS THEREOF
; FILE REFERENCE: MOA-A02051-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; PRIOR FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: Patent Ver. 2.1
; SEQ ID NO 5864
; LENGTH: 1027
; TYPE: DNA
; ORGANISM: Oryza sativa
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AK063027
; DATABASE ENTRY DATE: 2001-12-06
US-10-449-902-5864

Query Match 18.6%; Score 227.6; DB 6; Length 1027;
Best Local Similarity 66.7%; Pred. No. 1,1e-41;
Matches 340; Conservative 0; Mismatches 169; Indels 1; Gaps 1;

77 CAATGGGAGGAGGCTCCGCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 136
56 CGATGGGAGAGAGTGGCGGTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 115
137 AG 196
116 AG 175
197 TGGCCAG 256
176 TCCCAAG 235
257 ACCTGCGCGGAG 316
236 ACCTGCGCGGAG 295
317 ATTCAG 376
296 AGCTCCAG 355
377 CCGAG 435
356 CCGAG 415
436 GCTCAG 495
416 GCCTGAG 475
496 AAG 555
476 ACCTGCGCGGAG 535
556 TCGGAG 585
536 GCAGCAG 565

RESULT 5
US-10-449-902-8691
; Sequence 8691, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agricultural Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USBS THEREOF
; FILE REFERENCE: MOA-A02051-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; PRIOR FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: Patent Ver. 2.1
; SEQ ID NO 8691
; LENGTH: 1139
; TYPE: DNA
; ORGANISM: Oryza sativa
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AK106039
; DATABASE ENTRY DATE: 2002-06-28
US-10-449-902-8691

Query Match 18.6%; Score 223.6; DB 6; Length 1139;
Best Local Similarity 68.8%; Pred. No. 8.7e-41;
Matches 307; Conservative 0; Mismatches 139; Indels 0; Gaps 0;

QY 79 ATGGGAGGAGGCTCTGCTGCGAAGAAAGTGGGGCTCAAGAAAGGTCATGAGCGCGGAG 138
DB 187 ATGGGAGGAGGCTCTGCTGCGAAGAAAGTGGGGCTCAAGAAAGGTCATGAGCGCGGAG 246
QY 139 GAGGACAAAGTCTGCTGCTGCGAAGAAAGTGGGGCTCAAGAAAGGTCATGAGCGCGGAG 198
DB 247 GAGGACAAAGTCTGCTGCTGCGAAGAAAGTGGGGCTCAAGAAAGGTCATGAGCGCGGAG 306
QY 199 CCGAAGCAAGCGGCTGCTGCTGCGAAGAAAGTGGGGCTCAAGAAAGGTCATGAGCGCGGAG 258
DB 307 CCGAAGCAAGCGGCTGCTGCTGCGAAGAAAGTGGGGCTCAAGAAAGGTCATGAGCGCGGAG 366
QY 259 CTGCGCGGAGGATCAAGCGGCTGCTGCTGCGAAGAAAGTGGGGCTCAAGAAAGGTCATGAGCGCGGAG 318
DB 367 CTGCGCGGAGGATCAAGCGGCTGCTGCTGCGAAGAAAGTGGGGCTCAAGAAAGGTCATGAGCGCGGAG 426
QY 319 CTGCGCGGAGGATCAAGCGGCTGCTGCTGCGAAGAAAGTGGGGCTCAAGAAAGGTCATGAGCGCGGAG 378
DB 427 CTGCGCGGAGGATCAAGCGGCTGCTGCTGCGAAGAAAGTGGGGCTCAAGAAAGGTCATGAGCGCGGAG 486
QY 379 GAGGACAAAGTCTGCTGCTGCGAAGAAAGTGGGGCTCAAGAAAGGTCATGAGCGCGGAG 438
DB 487 GAGGACAAAGTCTGCTGCTGCGAAGAAAGTGGGGCTCAAGAAAGGTCATGAGCGCGGAG 546
QY 439 CAGGCGGCTGCTGCTGCTGCGAAGAAAGTGGGGCTCAAGAAAGGTCATGAGCGCGGAG 498
DB 547 ATGAGCGGCTGCTGCTGCTGCGAAGAAAGTGGGGCTCAAGAAAGGTCATGAGCGCGGAG 606
QY 499 AAGCGCGGCTGCTGCTGCTGCGAAGAAAGTGGGGCTCAAGAAAGGTCATGAGCGCGGAG 524
DB 607 AAGCGCGGCTGCTGCTGCTGCGAAGAAAGTGGGGCTCAAGAAAGGTCATGAGCGCGGAG 632

RESULT 6
US-10-953-349-33713
; Sequence 33713, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 33713
; LENGTH: 1284
; TYPE: DNA
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (736)..(736)
; OTHER INFORMATION: n is a, c, g, or t
US-10-953-349-33713

Query Match 18.5%; Score 222.8; DB 6; Length 1284;
Best Local Similarity 78.8%; Pred. No. 1.4e-40;
Matches 279; Conservative 0; Mismatches 72; Indels 3; Gaps 1;
QY 77 CATGGGAGGAGGCTCTGCTGCGAAGAAAGTGGGGCTCAAGAAAGGTCATGAGCGCGGAG 133
DB 125 CATGGGAGGAGGCTCTGCTGCGAAGAAAGTGGGGCTCAAGAAAGGTCATGAGCGCGGAG 184
QY 134 CCGAGGAGGAGGCTCTGCTGCGAAGAAAGTGGGGCTCAAGAAAGGTCATGAGCGCGGAG 193
DB 185 CCGAGGAGGAGGCTCTGCTGCGAAGAAAGTGGGGCTCAAGAAAGGTCATGAGCGCGGAG 244
QY 194 CCGTGGCGGAGGAGGCTCTGCTGCGAAGAAAGTGGGGCTCAAGAAAGGTCATGAGCGCGGAG 253
DB 245 CCGTGGCGGAGGAGGCTCTGCTGCGAAGAAAGTGGGGCTCAAGAAAGGTCATGAGCGCGGAG 304
QY 254 ACTACTGGGCGGAGGAGGCTCTGCTGCGAAGAAAGTGGGGCTCAAGAAAGGTCATGAGCGCGGAG 313

DB 305 ACTACTGGGCGGAGGAGGCTCTGCTGCGAAGAAAGTGGGGCTCAAGAAAGGTCATGAGCGCGGAG 364
QY 314 TCATCTCCAGAGGCTCTGCTGCGAAGAAAGTGGGGCTCAAGAAAGGTCATGAGCGCGGAG 373
DB 365 TCATCTCCAGAGGCTCTGCTGCGAAGAAAGTGGGGCTCAAGAAAGGTCATGAGCGCGGAG 424
QY 374 GAGGACAAAGTCTGCTGCTGCGAAGAAAGTGGGGCTCAAGAAAGGTCATGAGCGCGGAG 427
DB 425 GAGGACAAAGTCTGCTGCTGCGAAGAAAGTGGGGCTCAAGAAAGGTCATGAGCGCGGAG 478

RESULT 7
US-10-449-902-7552
; Sequence 7552, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agricultural Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A02051-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7552
; LENGTH: 1389
; TYPE: DNA
; ORGANISM: Oryza sativa
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AK064679
; DATABASE ENTRY DATE: 2001-12-06
US-10-449-902-7552

Query Match 18.1%; Score 217.8; DB 6; Length 1389;
Best Local Similarity 76.5%; Pred. No. 1.8e-39;
Matches 267; Conservative 0; Mismatches 82; Indels 0; Gaps 0;
QY 78 AATGGGAGGAGGCTCTGCTGCGAAGAAAGTGGGGCTCAAGAAAGGTCATGAGCGCGGAG 137
DB 149 AATGGGAGGAGGCTCTGCTGCGAAGAAAGTGGGGCTCAAGAAAGGTCATGAGCGCGGAG 208
QY 138 GAGGACAAAGTCTGCTGCTGCGAAGAAAGTGGGGCTCAAGAAAGGTCATGAGCGCGGAG 197
DB 209 GAGGACAAAGTCTGCTGCTGCGAAGAAAGTGGGGCTCAAGAAAGGTCATGAGCGCGGAG 268
QY 198 GCGGACAAAGGCTCTGCTGCGAAGAAAGTGGGGCTCAAGAAAGGTCATGAGCGCGGAG 257
DB 269 GCGGACAAAGTCTGCTGCTGCGAAGAAAGTGGGGCTCAAGAAAGGTCATGAGCGCGGAG 328
QY 258 CCGTGGCGGAGGAGGCTCTGCTGCGAAGAAAGTGGGGCTCAAGAAAGGTCATGAGCGCGGAG 317
DB 329 CCGTGGCGGAGGAGGCTCTGCTGCGAAGAAAGTGGGGCTCAAGAAAGGTCATGAGCGCGGAG 388
QY 318 TCTTCAGAGGCTCTGCTGCGAAGAAAGTGGGGCTCAAGAAAGGTCATGAGCGCGGAG 377
DB 389 TCTTCAGAGGCTCTGCTGCGAAGAAAGTGGGGCTCAAGAAAGGTCATGAGCGCGGAG 448
QY 378 GAGGACAAAGTCTGCTGCTGCGAAGAAAGTGGGGCTCAAGAAAGGTCATGAGCGCGGAG 426
DB 449 GAGGACAAAGTCTGCTGCTGCGAAGAAAGTGGGGCTCAAGAAAGGTCATGAGCGCGGAG 497
RESULT 8
US-10-449-902-2899
; Sequence 2899, Application US/10449902
; Publication No. US20060123505A1

```
GENERAL INFORMATION:
APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2899
LENGTH: 1037
TYPE: DNA
ORGANISM: Oryza sativa
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AK060684
DATABASE ENTRY DATE: 2001-12-06
US-10-449-902-2899
```

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Query Match      18.1%; Score 217.6; DB 6; Length 1037;
Best Local Similarity 59.5%; Pred. No. 1.8e-39;
Matches 389; Conservative 0; Mismatches 259; Indels 6; Gaps 1;
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QY 79 ATGGGAGAGGCTCCGTCTGCGAGAAAGATGGGCTCAGAGAGGCTCATGAGCCCGAG 138
DB 97 ATGGGAGAGGCTCCGTCTGCGAGAAAGATGGGCTCAGAGAGGCTCATGAGCCCGAG 156
QY 139 GAGGACAGAGTCTCTGCGCCCATTCACAGCCGACGCGCAATGGGCGCCCTG 198
DB 157 GAGGACAGAGTCTCTGCGCCCATTCACAGCCGACGCGCAATGGGCGCCCTG 216
QY 199 CCCAAGCAGAGCGGCGCTGCTGCGGCAAGAGCTGCGGCTCGGCTGAGCACTCA 258
DB 217 CCCAAGCAGAGCGGCGCTGCTGCGGCAAGAGCTGCGGCTCGGCTGAGCACTCA 276
QY 259 CTGCGGCGGAGATCAAGCGGCGCACTTCTCCAAAGAGAGAGAGACCATCATCAT 318
DB 277 CTGCGGCGGAGATCAAGCGGCGCACTTCTCCAAAGAGAGAGAGACCATCATCAT 336
QY 319 CTTCAGAGAGCTGCTGGGCAACAGTGTGCTCGCAATTCGCGCCAGGTTGCCG 378
DB 337 CTTCAGAGAGCTGCTGGGCAACAGTGTGCTCGCAATTCGCGCCAGGTTGCCG 396
QY 379 GACACAGAGATCAAGAACTGAGGACAGGACATCAAGCGCAAGCTCTGAGCCG 438
DB 397 GACACAGAGATCAAGAACTGAGGACAGGACATCAAGCGCAAGCTCTGAGCCG 456
QY 439 CAGGCGGTCTATGT-----CGGCGAGAGCGGCGGCGCAAGAGACCAAGAGC 492
DB 457 ATTCAGACCCGACAGCGAGCGGCGGTCTACGCGCGGAGAGAGCGCCCGCGG 516
QY 493 GCGAAGAGCCAGCGCGCGCGCGCGCGCGCGCGCGCGCTGCGCGAGCGGTCCG 552
DB 517 CTGACACAGAGCGGCGAGCAGCGCGCGCTTCTCCCTTGGCGCGCGCGCGCG 576
QY 553 TGTGCGGTGACGAGAGCTCTGAGTGGGCTGCTGCGGAGAGAGAGAGAGAGAG 612
DB 577 CAGCAGAGCTTACACAAACCGGAGAGCGCGCGCGCGCGCGAGATCGAGCTTCC 636
QY 613 ATTCAGCTCGGCGCTCCGCTGCTGCTGCGCGCAAGAGAGAGAGAGAGAGAG 672
DB 637 TCGCGGCGGTCCCGCGCGGTGAGAGAGCGGCAAGAGAGAGCGGCGAGCTGGA 696
QY 673 GAGGAGTTCCAGATGACAGACAGCTTCTGCTCGGAGAGAGCTGTCAGTCCG 726
DB 697 CCGCGGTGCGCGAGCTCAACCTGAGCTGAGCTGAGCTGCTGAGCTGAGCTG 750
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RESULT 9
US-10-449-902-26232
Sequence 26232, Application US/10449902
Publication No. US20060123505A1
GENERAL INFORMATION:
APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 26232
LENGTH: 995
TYPE: DNA
ORGANISM: Oryza sativa
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AK101674
DATABASE ENTRY DATE: 2002-08-28
US-10-449-902-26232
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Query Match      18.1%; Score 217.4; DB 6; Length 995;
Best Local Similarity 76.7%; Pred. No. 1.9e-39;
Matches 266; Conservative 0; Mismatches 81; Indels 0; Gaps 0;
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QY 71 CAAGCAATAGGAGAGGCTCCGTCTGCGAGAAAGATGGGCTCAGAGAGGCTCAT 130
DB 109 CATCGACATGAGTGAAGCGCGCGCTGCGAGCAAGAGACGCGTCAAGAGGCG 168
QY 131 CGCGGAGAGAGCAAGAGTCTGCTGCGCCATTCAGAGCGCGCAAGAGAGAG 190
DB 169 CGCGGAGAGAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 228
QY 191 GCGGCTGCGCCAGAGAGCGGCGCTGCTGCGGCAAGAGCTGCGGCTCGGTTGA 250
DB 229 GCGGCTGCGCCAGAGAGCGGCGCTGCTGCGGCAAGAGCTGCGGCTCGGTTGA 288
QY 251 TCAACTACTGCGGCGCGGCAATCAAGCGGCGCACTTCTCAGAGAGAGAGACA 310
DB 289 CCAACTACTGAGGCGCGGAGATCAAGCGGCGGAACTTCAAGCGAGAGAGAG 348
QY 311 TCATCATCTCAGAGAGCTGCTTGGCAAGAGTGTCCGCAATTCGCGAGGTTG 370
DB 349 TGTCACTCTCAGAGAGCTGCTTGGCAAGAGTGTCCGCAATTCGCGAGGTTG 408
QY 371 GAGGAGAGAGAGAGATCAAGAGAGTGTGAGAGAGAGAGAGAGAGAGAGAG 417
DB 409 AGGAGAGAGAGAGAGATCAAGAGAGTGTGAGAGAGAGAGAGAGAGAGAGAG 455
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```
RESULT 10
US-10-449-902-3902
Sequence 3902, Application US/10449902
Publication No. US20060123505A1
GENERAL INFORMATION:
APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: JP 2002-383870
```

PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3902
LENGTH: 1087
TYPE: DNA
ORGANISM: Oryza sativa
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AK061437
DATABASE ENTRY DATE: 2001-12-06
US-10-449-902-3902

Query Match
Best Local Similarity 75.1%; Pred. No. 2,4e-39;
Matches 271; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

18.1%; Score 217; DB 6; Length 1087;
77 CAATGGGAGGAGCTCCGTGCTGGAGAGATGGGCTCAAGAGGGTCCATGAGCGCG 136
107 CCATGGGCGGCGCGCTGCTGGAGAGAGAGGGATCAAGAGGGGCGATGAGCGCG 166
QY 137 AGGAGGACAGGTCTCTGCTGCGGCAATCCAGCGCCACCGGCACTGGCGCGCC 196
DB 167 AGGAGGACATCTCTCTGCTGCTCAATCCAGAGACCGCCCGGCACTGAGATCG 226
QY 197 TGCCCAAGCAAGCGGCGCTGCTGCGGCAAGAGCTGCGGCTCCGATGATCACT 256
DB 227 TTCCCATCAACTGCGGCTGATGAGTGAAGCAAGAGCTGAGGCTGCGGATGAG 286
QY 257 ACCTGGGCGGAGATCAAGACGGGCGCACTTCTCAAGAGAGAGACACCATCATC 316
DB 287 ACCTGGGCGGAGATCAAGACGGGCGCACTTCAAGAGAGAGAGAGAGAGATCAT 346
QY 317 ATCTCCAGAGCTGCTGCTGCGCAACAGTGTGCTGCAATTCGCCGAGTGGCCG 376
DB 347 ACCTCCAGTGTCTTCTGCGCAACCGCTGCGCGCATCTCTCACTCCCGGAG 406
QY 377 CGGACAGAGATCAAGAGAGTGTGCGACACCCAGCTCAAGAGCGCTGATGCGCG 436
DB 407 CGGACAGAGATCAAGAGAGTGTGCGACACCCAGCTCAAGAGAGAGCTGCGCG 466

QY 437 C 437
DB 467 C 467

RESULT 11
US-10-449-902-11361

Sequence 11361, Application US/10449902
Publication No. US20060123505A1
GENERAL INFORMATION:

APPLICANT: National Institute of Agricultural Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF.

FILE REFERENCE: MOA-A02051-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 11361
LENGTH: 1031
TYPE: DNA
ORGANISM: Oryza sativa
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AK108709
DATABASE ENTRY DATE: 2002-08-28
US-10-449-902-11361

Query Match
Best Local Similarity 17.7%; Score 212.4; DB 6; Length 1031;
Matches 264; Conservative 0; Mismatches 86; Indels 0; Gaps 0;

QY 79 ATGGGAGGAGCTCCGTGCTGGAGAGATGGGCTCAAGAGGTCATGAGCGCGAG 138
DB 87 ATGGGAGGAGAGCTGCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 146
QY 139 GAGGACAGAGCTCTGCTGCGGCAATCCAGCGCCACCGGCACTGGCGCGCC 198
DB 147 GAGGACAGAGAGCTGCTCTCTCTCTCAATGAGCACTGCTGAGGCTGCTG 206
QY 199 CCAAGCAAGCGGCGCTGCTGCTGCGGCAAGAGAGAGAGAGAGAGAGAGAG 258
DB 207 CCAAGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 266
QY 259 CTGGGCGGAGATCAAGCGGCGCACTTCTCAAGAGAGAGAGAGAGAGAGAG 318
DB 267 CTGGGCGGAGATCAAGCGGCGCACTTCTCAAGAGAGAGAGAGAGAGAGAG 326
QY 319 CTGCAAG 378
DB 327 CTGCAAG 386
QY 379 GACAAGAGATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 428
DB 387 GACAAGAGATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 436

RESULT 12

US-10-449-902-1122
Sequence 1122, Application US/10449902
Publication No. US20060123505A1
GENERAL INFORMATION:

APPLICANT: National Institute of Agricultural Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF.

FILE REFERENCE: MOA-A02051-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1122
LENGTH: 1042
TYPE: DNA
ORGANISM: Oryza sativa
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AK104053
DATABASE ENTRY DATE: 2002-08-28
US-10-449-902-1122

Query Match
Best Local Similarity 17.5%; Score 209.8; DB 6; Length 1042;
Matches 350; Conservative 0; Mismatches 192; Indels 15; Gaps 1;

QY 77 CAATGGGAGGAGCTCCGTGCTGGAGAGATGGGCTCAAGAGGTCATGAGCGCG 136
DB 132 CCATGGGAGGAGCTGCTGCTGCGGCAATCCAGCGCCACCGGCACTGGCGCG 191
QY 137 AGGAGGACAGGTCTCTGCTGCGGCAATCCAGCGCCACCGGCACTGGCGCG 196
DB 192 AGGAGGACAGGCTCTCTGCTGCGGCAATCCAGCGCCACCGGCACTGGCG 251
QY 197 TGCCCAAGAGAGCGGCGCTGCTGCGGCAATCCAGCGCCACCGGCACTGGCG 256
DB 252 TGCCCAAGAGAGCGGCGCTCTCTGCTGCGGCAATCCAGCGCCACCGGCACT 311

Oy	257	ACCTGCGGCCGGAATCAAGCGGGGACATTTCGAAAGGAGGAGGACCATCATCC	316
Db	312	AACCTCCGCCGACTTCAAGCGGGCATTTCACGACGAGGAGGAGACTATATCC	371
Oy	317	ATCTCCAGAGTGCTGTGGCAAAGGTGTCGCATATTCGCGCAAGTTGCCCGGAGGA	376
Db	372	GCTTCCAAGCTCCTCGGCAACAAGTGTCTCTGTATTCGCCGGGCGAGTGGCGGGAGGA	431
Oy	377	CGGACATCGAAGTCAAGAAGTGTGGCACACCACCTTAAGANG-----	421
Db	432	CGGACAAAGAGATCAAGAACTACTGGAACGCACTCAAGCGCAAGCTCTGCCCGG	491
Oy	422	GCCTGATGCGCGGGGTACGGGCGGTGATGTGGCGCGAGCGCGCGCAAGACACAAG	481
Db	492	GCAITGACCCCGAGAGCGACCGCCCGCTGCTCAAGCGCGGTGACGGCATTCGCGGAGCA	551
Oy	482	AGCCGAAGAGCGCGAAGAGCCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAGC	541
Db	552	ACAAGGGCGGACCAACGCGCGCGCGCATTCATATTCCTCCCGGGAAGCGCGCGCGG	611
Oy	542	GSTCGGCTCTGTCGTGAGCGAGTCTCGATGCGCTGTCGATGGCGGAGAGACAG	601
Db	612	CGATTTTCGCGGTGCGAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCTCTCGAGCAGC	671
Oy	602	GCACGCGCGGATCAGC	618
Db	672	GCTGCGGAGCGAGC	688

```

RESULT 13
US-10-449-902-16336
: Sequence 16336, Application US/10449902
: Publication No. US20060123505A1
: GENERAL INFORMATION:
: APPLICANT: National Institute of Agrobiological Sciences.
: APPLICANT: Bio-oriented Technology Research Advancement Institution.
: APPLICANT: The Institute of Physical and Chemical Research.
: APPLICANT: Foundation for Advancement of International Science.
: TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
: FILE REFERENCE: MOA-A0205Y1-US
: CURRENT APPLICATION NUMBER: US/10/449,902
: CURRENT FILING DATE: 2003-05-29
: PRIOR APPLICATION NUMBER: JP 2002-203269
: PRIOR FILING DATE: 2002-05-30
: PRIOR APPLICATION NUMBER: JP 2002-383870
: PRIOR FILING DATE: 2002-12-11
: NUMBER OF SEQ. ID NOS: 56791
: SOFTWARE: Patentin Ver. 2.1
: SEQ ID NO 16336
: LENGTH: 1069
: TYPE: DNA
: ORGANISM: Oryza sativa
: PUBLICATION INFORMATION:
: DATABASE ACCESSION NUMBER: AK066634
: DATABASE ENTRY DATE: 2001-12-06
: US-10-449-902-16336

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Query Match	17.5%	Score 209.8;	DB 6;	Length 1069;
Best Local Similarity	62.8%	Pred. No. 9.5e-38;		
Matches 350;	Conservative 0;	Mismatches 192;	Indels 15;	Gaps 1

[illegible]

Oy	257	ACCTGCGGCGGGAATCAAGGCGGGCACTTCTCCAGGAGGAGGACACATCATCC	316
Db	317	ACCTCGCCCCGCACTCAAGGCGGCACTTACCGACGACGAGGACGACTATATATCC	376
Oy	317	ATCTCCACGAGCTGTTGGCAACAGATGATGCGCAATTGCCGCAAGTGTGCCCGGAGGA	376
Db	377	GCTTCACAGCTCTCTGGCAACAGTGTGTCTATATGCTCGGGGAGCTGCGGGGAGGA	436
Oy	377	CGGACACGAGATCAAGAACGTGTGGCACCCCACTTCAAGAAC-----421	
Db	437	CGGACACGAGATCAAGAACTACTGTGAACCGCACATCAAGGCGCAAGCTCTTGCCCGCG	496
Oy	422	GGCTCGATGGCGCGGCTCAGGGCGGTCAATGTGGGGCGGCGGGCGGCAAGACACAAG	481
Db	497	GCATGTACCCCGAAGCGCACCGCCCGCTGTGTAGCGGCGGTATACCGCATTCGGCGAGCA	556
Oy	482	AGCCGAAGAGCGCGAAGAACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAGC	541
Db	557	ACAAAGGCGGACACACCGCGCGCGCATTCATATCCGTCCCGGCGAAGGCGGCGCGCGG	616
Oy	542	GGTCCGCTCGTCTCGGTGAACGAGTCTTCGATGAGCTCTGTCGGTGGCGAGAGACAG	601
Db	617	CGATCTTTCGCGGTGGCGAAGCGCGCGCACCGCGCGCGCGGTTCGACTCTCGACGACG	676
Oy	602	GCAACGCCGGGATCAGC	618
Db	677	GCTCCCGGACGACGAC	693

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US RESULT 4 US/10449-902-19393
Sequence 19393, Application US/10449902
Publication No. US20060123505A1
GENERAL INFORMATION:
APPLICANT: National Institute of Agrobiol
APPLICANT: Bio-oriented Technology Resea
APPLICANT: The Institute of Physical and
APPLICANT: Foundation for Advancement of
TITLE OF INVENTION: FULL-LENGTH PLANT CDN
FILE REFERENCE: MOA-A0205V1-US
CURRENT APPLICATION NUMBER: US/10/449, 902
CURRENT FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: JP 2002-203265
PRIOR FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 19393
LENGTH: 1023
TYPE: DNA
ORGANISM: Oryza sativa
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AK099108
DATABASE ENTRY DATE: 2002-08-28
US-10-449-902-19393

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Query Match	17.3%	Score 208.2;	DB 6;	Length 1023;
Best Local Similarity	62.7%;	Pred. No. 2.1e-37;		
Matches 349;	Conservative 0;	Mismatches 193;	Indels 15;	Gaps 1;

QY	77	CAAATGGGGAGGGGCTCCGCTGTCAGAAAGATGGGGCTCAAGAAAGATCATATGACGCCG	136
Db	141	CCATGGGGAGGTCCCGCTGTCGCGAAGAGCGCACACGCAACCAAGGGGGGCTGTGACCAAG	200
QY	137	AGAGAGCAAGAGTCCTGTCGCCCAATCCACGCGCAGAGGCTACGAGCAATGTGGCGGCC	196
Db	201	AGAGAGCAAGAGGCTCATGCGGTACATCAAGACAGGGCGCACATGGCGAAGAGCTGTGGCGCTGCC	260
QY	197	TGCCCCAAGCAAGCCGGGCTGTGCTGGTTGCGGCAAGAGCTGCCGGCTCTCGGTGTGATCAACT	256
Db	261	TGCCCAAGAGCGCGGGGCTCTCTTGTGCTGGCGGCAAGAGCTGTGCGCTCTCGGTGTGATCAACT	320


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QY 257 ACCTGCGCCGGAATCAAGCGGGCACTTCTCAAGAGAGAGACACCATCATCC 316
DB 321 ACCTCGCCCGCTCAAGCGGGCACTTCAAGAGAGAGAGAGAGAGAGAGAGAG 380
QY 317 ATCTTCACGAGCTGCTTGGCAACAGGTGGTCCGCAATTCGCCAGTTGCCGAGAG 376
DB 381 GCTTCACAGCTCTCTCGGCAACAGGTGGTCTCTGATTCGCCGAGAGAGAGAGAG 440
QY 377 CGGACACGAGATCAAGAACTGTGGCACACCACTCTCAAGAGC----- 421
DB 441 CGGACACGAGATCAAGAACTGTGGAACACGACATCAAGAGAGAGAGAGAGAG 500
QY 422 GCTTCGAGTGGCGGGGTCAAGTGTGATGTGCGGCGAGCGGGCAAGAGAGAGAG 481
DB 501 GATTCGACCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 560
QY 482 AGCCGAAGAGCGCGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 541
DB 561 AGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 620
QY 542 GGTCCGCTCTGTCGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 601
DB 621 CGATCTTCGCGGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 680
QY 602 GCAAGCGCGGATCAGC 618
DB 681 GCTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 697
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RESULT 15

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US-10-449-902-3635
; Sequence 3635, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agricultural Sciences.
; APPLICANT: Bio-Oriented Technology Research Advancement Institution.
; APPLICANT: Foundation for Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A02051-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 3635
; LENGTH: 1048
; TYPE: DNA
; ORGANISM: Oryza sativa
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AK104457
; DATABASE ENTRY DATE: 2002-08-28
US-10-449-902-3635
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Query Match 16.9%; Score 203; DB 6; Length 1048;

Best Local Similarity 74.1%; Pred. No. 3e-36;

Matches 257; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

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QY 79 ATGGGAGAGGCTCCGCTGTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 138
DB 94 ATGGGAGAGGCTACCGCTGTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 153
QY 139 GAGGACAGAGCTCTGTCGCAATCAAGCGGCAAGGCAAGGCAAGGCAAGGCTG 198
DB 154 GAAAGATGACCGGCTCATGCTCAATCAAGCGGCAAGGCAAGGCAAGGCAAGGCTG 213
QY 199 CCCAAGCAGCGGGGCTGCTGCTGCGGCAAGAGAGAGAGAGAGAGAGAGAGAG 258
DB 214 CCCAAGCAGCGGGGCTCTCTGCTGTCGCAAGAGAGAGAGAGAGAGAGAGAG 273
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QY 259 CTGCGGCGGAGCATCAAGCGGGCAACTTCTCAAGAGAGAGAGAGAGAGAGAG 318
DB 274 CTGCGGCTTGAAGCTTCAAGCGGGCAACTTCAAGAGAGAGAGAGAGAGAGAG 333
QY 319 CTCAAGAGCTGCTTGGCAACAGGTGGTCCGCAATTCGCCAGTTGCCGAGAGAG 378
DB 334 CTTCAGAGCTTTTGAAGCAAGATGCTCTGATAGCCGGGAGGTTGCCAGAGAGAG 393
QY 379 GACACGAGATCAAGAACTGTGGCACACCACTCTCAAGAGAGAGAGAGAGAG 425
DB 394 GACACGAGATCAAGAACTGTGGAACACGACATCAAGAGAGAGAGAGAGAGAG 440
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Search completed: June 25, 2006, 08:02:34
Job time : 49 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 24, 2006, 00:04:48 ; Search time 186 Seconds

(without alignments)
640.033 Million cell updates/sec

Title: US-10-521-811-2

Perfect score: 1368
Sequence: 1 MGAPPCCKKGLKKGWTPF.....MDYLVGFMSGEADLPQI 257

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 209797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 209797

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA Main:
1: /EMC_Celerra_SIDS3/prodata/2/pubppaa/US07_PUBCOMB.pep.*
2: /EMC_Celerra_SIDS3/prodata/2/pubppaa/US08_PUBCOMB.pep.*
3: /EMC_Celerra_SIDS3/prodata/2/pubppaa/US09_PUBCOMB.pep.*
4: /EMC_Celerra_SIDS3/prodata/2/pubppaa/US10_PUBCOMB.pep.*
5: /EMC_Celerra_SIDS3/prodata/2/pubppaa/US10_PUBCOMB.pep.*
6: /EMC_Celerra_SIDS3/prodata/2/pubppaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1368	100.0	257	4 US-10-437-963-122749	Sequence 122749,
2	920	67.3	229	4 US-10-425-115-222820	Sequence 222820,
3	892	65.2	279	4 US-10-425-115-343620	Sequence 343620,
4	835.5	61.1	288	6 US-11-087-099-10942	Sequence 10942, A
5	827.5	60.5	258	3 US-09-443-704-4	Sequence 4, Appl1
6	827.5	60.5	258	4 US-10-008-118A-4	Sequence 4, Appl1
7	827.5	60.5	258	4 US-10-437-963-192931	Sequence 192931,
8	799.5	58.4	257	6 US-11-096-568A-25633	Sequence 25633, A
9	799.5	58.4	257	6 US-11-096-568A-25633	Sequence 25633, A
10	793.5	58.0	261	4 US-10-425-115-335937	Sequence 335937, A
11	769	56.2	241	4 US-10-425-115-337771	Sequence 237771,
12	747.5	54.9	248	6 US-11-087-099-1043	Sequence 1043, A
13	709.5	51.6	280	6 US-11-087-099-1043	Sequence 211312,
14	707	51.7	200	4 US-10-437-963-122749	Sequence 122749,
15	697.5	51.0	276	4 US-10-437-963-110428	Sequence 110428,
16	694	50.7	281	6 US-11-087-099-11569	Sequence 11569, A
17	690	50.4	281	6 US-11-087-099-1364	Sequence 3364, A
18	687	50.2	265	6 US-11-087-099-12004	Sequence 12004, A
19	684	50.0	277	4 US-10-374-780A-569	Sequence 569, App
20	684	50.0	277	6 US-11-087-099-8475	Sequence 8475, App
21	669.5	48.9	278	6 US-11-087-099-4872	Sequence 4872, App
22	661.5	48.4	304	4 US-10-425-114-54105	Sequence 54105, A
23	658	48.1	275	4 US-10-424-599-111312	Sequence 111312,
24	658	48.1	313	4 US-10-425-114-40952	Sequence 40952, A
25	653.5	47.8	253	6 US-11-087-099-8762	Sequence 8762, App
26	647	47.3	258	4 US-10-425-115-23688	Sequence 23688,
27	646.5	47.3	253	6 US-11-087-099-11259	Sequence 11259, A

28	642.5	47.0	171	4 US-10-425-115-211744	Sequence 211744,
29	640	46.8	273	3 US-09-533-029-62	Sequence 62, App1
30	640	46.8	273	4 US-10-278-173-140	Sequence 140, App
31	640	46.8	273	4 US-10-278-536-58	Sequence 58, App1
32	640	46.8	273	4 US-10-225-066A-776	Sequence 776, App
33	640	46.8	273	4 US-10-374-780A-40	Sequence 40, App1
34	640	46.8	273	4 US-10-374-780A-1978	Sequence 1978, App
35	640	46.8	273	4 US-10-412-699B-156	Sequence 156, App
36	640	46.8	273	4 US-10-412-699B-154	Sequence 154, App
37	640	46.8	273	4 US-10-412-699B-1754	Sequence 1754, App
38	640	46.8	273	5 US-10-225-066A-776	Sequence 776, App
39	640	46.8	276	5 US-10-958-411-2	Sequence 2, Appl1
40	626.5	45.8	139	3 US-09-443-704-38	Sequence 38, App1
41	626.5	45.8	139	4 US-10-008-118A-38	Sequence 38, App1
42	623.5	45.6	246	4 US-10-412-699B-116	Sequence 116, App
43	605.5	44.3	199	4 US-10-424-599-267017	Sequence 267017,
44	601	43.9	249	4 US-10-278-173-22	Sequence 22, App1
45	601	43.9	249	4 US-10-412-699B-822	Sequence 822, App

ALIGNMENTS

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RESULT 1
US-10-437-963-122749
; Sequence 122749, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovacic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437, 963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 122749
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_25649C.1.pep
US-10-437-963-122749

Query Match      100.0%; Score 1368; DB 4; Length 257;
Best Local Similarity 100.0%; Pred. No. 8.2e-11;
Matches 257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MGAPPCCKKGLKKGWTPEDKVLVAHIOHGHGMRLLPKQAGLLRGSKRLRWNY 60
Db 1 MGAPPCCKKGLKKGWTPEDKVLVAHIOHGHGMRLLPKQAGLLRGSKRLRWNY 60
Oy 1 LRDPDRGNFSKEEDTIHILHLLGNRWSAIAARLPGRTDNEIKVWHTLTKRLDAPA 120
Db 1 LRDPDRGNFSKEEDTIHILHLLGNRWSAIAARLPGRTDNEIKVWHTLTKRLDAPA 120
Oy 1 QGGHVAASGGKHKRKRSAKPPAAAAAPPASPERASSSVYBSSVAABHGNAGIS 180
Db 1 QGGHVAASGGKHKRKRSAKPPAAAAAPPASPERASSSVYBSSVAABHGNAGIS 180
Oy 1 SASASVCAKESSFTSASEEFOIDSFWSFTLSMPIDGVSWEPGDAFVAPPSADMDY 240
Db 1 SASASVCAKESSFTSASEEFOIDSFWSFTLSMPIDGVSWEPGDAFVAPPSADMDY 240
Oy 1 WLGVMESGEADLPQI 257
Db 1 WLGVMESGEADLPQI 257
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```
RESULT 2
US-10-425-115-222820
; Sequence 222820, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425.115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 222820
; LENGTH: 295
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_134802C.1.pep
US-10-425-115-222820

Query Match          67.3%; Score 920; DB 4; Length 295;
Best Local Similarity 67.3%; Pred. No. 5.2e-73;
Matches 202; Conservative 9; Mismatches 41; Indels 48; Gaps 12;

QY 1 MGRAPCEKMGKKGKGPWTEEDKVLVAHIQRHGHGNWRALPKOAGLLRCGSKCRLRWINY 60
DB 1 MGRAPCEKMGKKGKGPWTEEDKVLVAHIQSFHGNWRALPKOAGLLRCGSKCRLRWINY 60
QY 61 LRPDIKRGNFSKEEDTITLHLELGNRWSAIAARLPGRTDNEIKVWHTLKKRLDAPA 120
DB 61 LRPDIKRGNFSKEEDAIITLHLELGNRWSAIAARLPGRTDNEIKVWHTLKKRLDPTK 120
QY 121 Q-----GGHVAASGGKKHKKPSAKK-----PA-AAAAAPSPERS 156
DB 121 QEQQOQHGTTPAAGAGKGRPAALAAKRGCGGAKATANADAVVPAAPATAAPSPERS 180
QY 157 -ASSSVTESSMASSVAEHEGNAGISSASASVCAKESSPTSAS--EEFOIDSFMSSETLS 213
DB 181 AASSSVTESSMTQ--EQEHNTGSSPA---FPKEESTLTTSSSDAEFPQDFDSFMSSETLS 235
QY 214 MPIDGTD--VSMPPG-DAF-----VAPPSAD-----DMDYVLGVFMESGEA-Q-DLPQI 257
DB 236 MPIDSLDDVVPMEPSDDAFGDVDVDVAASSSSVGADGDLDWLRFVMEGSDAHPQLPQI 295

RESULT 3
US-10-425-115-343620
; Sequence 343620, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425.115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 343620
; LENGTH: 279
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(279)
; OTHER INFORMATION: unsure at all Xaa locations
```

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; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_76543C.1.pep
US-10-425-115-343620

Query Match          65.2%; Score 892; DB 4; Length 279;
Best Local Similarity 64.6%; Pred. No. 1.5e-70;
Matches 186; Conservative 18; Mismatches 44; Indels 40; Gaps 11;

QY 1 MGRAPCEKMGKKGKGPWTEEDKVLVAHIQRHGHGNWRALPKOAGLLRCGSKCRLRWINY 60
DB 1 MGRAPCEKMGKKGKGPWTEEDKVLVAHIQSFHGNWRALPKOAGLLRCGSKCRLRWINY 60
QY 61 LRPDIKRGNFSKEEDTITLHLELGNRWSAIAARLPGRTDNEIKVWHTLKKRLDAPA 120
DB 61 LRPDIKRGNFSKEEDAIITLHLELGNRWSAIAARLPGRTDNEIKVWHTLKKRLDPTT 120
QY 121 Q-----GGHVAASGGKKHKKPSA---KPPAAAAAP-----PASPERS-ASSSVTESS 165
DB 121 KOLEQEOHGAHAGDPAARKRSPKRAAXKTTTAAVAPATTAAPASPERSAASSSVTEST 180
QY 166 MASSVAEHEGNAGISSASASVCAKESSPTS--ASEFOIDSFMSSETLSMPIDGY-DV 221
DB 181 ----EQEGNTGTSSPG---FPKEESTSSSEAEERFQDFDTFMSSETLSMPIDSFDDV 231
QY 222 SMEP-----GDAFYAAPPSAD-----DMDYVLGVFMESGEA-QDLPQI 257
DB 232 PTEPCSSGAFGDVVAASSSSSVGDADLDYWLGVFMKSGDAHQQLPQV 279
```

```
RESULT 4
US-11-087-099-10942
; Sequence 10942, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 10942
; LENGTH: 288
; TYPE: PRT
; ORGANISM: Hordeum vulgare
US-11-087-099-10942

Query Match          61.1%; Score 835.5; DB 6; Length 288;
Best Local Similarity 64.7%; Pred. No. 1.6e-65;
Matches 180; Conservative 12; Mismatches 47; Indels 39; Gaps 7;
```

```
QY 16 PWTPEEDKVLVAHIQRHGHGNWRALPKOAGLLRCGSKCRLRWINYLRPIKGNFSKEE 75
DB 14 PYDAAECKTLVAHIHSHGHGNWRALPKOAGLLRCGSKCRLRWINYLRPIKGNFSDEE 73
QY 76 DTIILHLELGNRWSAIAARLPGRTDNEIKVWHTLKKRLDAPAQGVAAASGGKQHK 135
DB 74 QSTIQHLQHLGNRWSAIAARLPGRTDNEIKVWHTLKKRLDPSAQEQEBAKAKRK 133
QY 136 PKSAK-----KRAAAAAAPASPERASSTYTES-SMASSVAEHEGN 176
DB 134 PAAAAAAPRKDGKVMRNLTARAAAAAVSSPERVSVSTYESTSTAABAOHGN 193
QY 177 AGISSASASVCAKESSPTS--SEFOIDSFMSSETLSMPIDGY-DVSMPPGDAFVAP 233
DB 194 SSSSSASASASYKE-CFTSSSESEEFQIDSEFMSSETLSMPIDLDLNDVCMERHDAFGKD 252
QY 234 SADMDYVLGVFMESG-----EAQDLPQI 257
DB 253 G--DMDYWLRLFMEGGSGSGSDNNNNHDGALDLPQI 288
```

```
RESULT 5
US-09-443-704-4
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Query Match	60.5%	Score	827.5	DB 4	Length	258	
Best Local Similarity	62.1%	Pred. No.	6.9e-65				
Matches 169, Conservative	29	Mismatches	45	Indels	29	Gaps	8

QY	230	VAPSA---	DDM-DYWLGVFMESEGAQDLDPOI	257
DB	227	GASPSNSDDDDMDDFWLKLEIAGGMONLDPOI	258	

```

RESULT 9
US-11-096-568A-25632
: Sequence 25632, Application US/11096568A
: Publication No. US20060048240A1
: GENERAL INFORMATION:
: APPLICANT: Alexandrov, Nikolai et al.
: TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
: TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
: FILE REFERENCE: 2750-1592PUS2
: CURRENT APPLICATION NUMBER: US/11/096,568A
: CURRENT FILING DATE: 2005-04-01
: NUMBER OF SEQ ID NOS: 34471
: SEQ ID NO 25632
: LENGTH: 309
: TYPE: PRT
: ORGANISM: Zea mays subsp. mays
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (1)..(309)
: OTHER INFORMATION: Ceres Seq. ID no. 15222886
US-11-096-568A-25632

```

Query Match	58.4%;	Score 799.5;	DB 6;	Length 309;
Best Local Similarity	58.8%;	Pred. No. 2.7e-62;		
Matches 160;	Conservative 30;	Mismatches 51;	Indels 31;	Gaps 8;

```

RESULT 10
US-10-425-115-335937
Sequence 335937, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425.115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 335937
LENGTH: 261
TYPE: PRT
ORGANISM: Zea mays
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(261)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
OTHER INFORMATION: Clone ID: MWT4577_69483C.1.pep
US-10-425-115-335937

```

Query	March	58.0%	Score 793.5	DB 4:	Length 261:
	Best Local Similarity	57.5%	Pred. No. 73	62:	
	Matches 157:	Conservative 31:	Mismatches 56:	Indels 29:	Gaps 7
QY	1	MGRAPCCCEKMLKKGPWTPTEEDKVLVAHIIQRHGHGNMRLPK-QAGLLRCGSKSCLRLWIN	59		
Db	1	MGRSPCCCKMLKKGPMTAEEDRLIVAAVERHGHNMNMLPKQAGLLRCGSKSCLRLWIN	60		
QY	60	YLRPDIKRGNSKEEDPTIILHETLLGRWSAIAARLPGRTNEAIKNVHTLKKRLDAP	119		
Db	61	YLRPDIKRGNSREEDDAIIQLHQLGNRMSTIAARLPGRTDNEAIKNVHTLKKRLLEPK	120		
QY	120	AAGGHVAASGKSKHKKPKSAKKPAA----AAAPASPERSAS--SSYTESMSSSVAE	172		
Db	121	PASQDAPKPKKTKKQOPPEPEPVYTLLEGPAVAPVPSERSLSTTSTTSTADYSAAS	180		
QY	173	EHGNAGISASASVCAKEESSFTSASEFOIDDSFMSSETLSM--PLDGDVMEIP-----	225		
Db	181	SLKNAQ-----DFTSEEDVYQIIDDSFMSSETLANTTYTVDSESGVQQAEGSF	227		
QY	226	GDADFVAPPSA-DMMDYLGVMESGEADLPPI	257		
Db	228	GKSAAPBSTDDMDFWLKLFMQASDMQNLPI	260		


```

; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 42619
; LENGTH: 200
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAV03-C81473_1.pep
US-10-767-701-42619
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Query Match          51.7%; Score 707; DB 4; Length 200;
Best Local Similarity 72.0%; Pred. No. 2,4e-54;
Matches 139; Conservative 7; Mismatches 35; Indels 12; Gaps 3;
```

```

QY      1 MGRAPCCCKMGLKGPWTPEDKVLVAHIQHGHNMRALPKOAGLLRCGKSCRLRWINY 60
        |||||||
DB      1 MGRAPCCCKMGLKGPWTPEDKVLVAHIQHGHNMRALPKOAGLLRCGKSCRLRWINY 60
        |||||||
QY      61 LRPDIKRGNSKEEDTIIHLHELGNRWSAIAARLPGRTDNEIKVWHTHLKKRLDAPA 120
        |||||||
DB      61 LRPDIKRGNSKEEDTIIHLHELGNRWSAIAARLPGRTDNEIKVWHTHLKKRLDAPA 120
        |||||||
QY      121 ----QGGHVAASGGKHKKKPKSAKKPAAA-----AAAPPAPEPS-ASSSTESSMAS 168
        |||||
DB      121 KPEEQHGAQAGAGKGRPRGAAKKTTADDAVAVPATTAPVSPERSPASSSVTESSSMT 180
        |||||
QY      169 SVAEEHGNAGISS 181
        :|||
DB      181 EOEQEGCNTGSSA 193
        :|||
```

```

RESULT 15
US-10-437-963-110428
; Sequence 110428, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 110428
; LENGTH: 276
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_14495C.1.pep
US-10-437-963-110428
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Query Match          51.0%; Score 697.5; DB 4; Length 276;
Best Local Similarity 53.2%; Pred. No. 2.5e-53;
Matches 150; Conservative 34; Mismatches 61; Indels 37; Gaps 10;
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```

QY      1 MGRAPCCCKMGLKGPWTPEDKVLVAHIQHGHNMRALPKOAGLLRCGKSCRLRWINY 60
        |||||||
DB      1 MGRAPCCCKMGLKGPWTPEDKVLVAHIQHGHNMRALPKOAGLLRCGKSCRLRWINY 60
        |||||||
QY      61 LRPDIKRGNSKEEDTIIHLHELGNRWSAIAARLPGRTDNEIKVWHTHLKKRLD--- 117
        |||||||
DB      61 LRPDIKRGNSKEEDTIIHLHELGNRWSAIAARLPGRTDNEIKVWHTHLKKRLD--- 120
        |||||||
```

```

QY      118 --APAQGGHVAASGGKK---HKPKSAKKPAAA---AAPPAPEPSAS---SSVTESSMA 167
        |||||
DB      121 KLAAGGG-----GARRPHTRKQPYAAKSAALVKEATPSVVDTSSTVTESS-P 174
        |||||
QY      168 SVAEEHGNAGISSASASVCAKESSFTSASE-----EFOIDSFWSET---LS 213
        |||||
DB      175 SSADGDHRRQOQOTQHAAY---KEESFSGGELPAAAAAFTAAADWDESFMSSTEVTKMM 231
        |||||
QY      214 MPLDGYDVSME--PGDAFVAAPPSADMDYVLGVFMESGEAODL 254
        |||||
DB      232 AGLDGMDDELATAGTSSAAAPASDDMEFWLKMILLEGDWRL 273
        |||||
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```

Search completed: June 24, 2006, 00:08:43
J00 time : 187 secs
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RESULT 2
US-10-953-349-9699
; Sequence 9699, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 9699
; LENGTH: 285
; TYPE: PRP
; ORGANISM: Arabidopsis thaliana
US-10-953-349-9699

Query Match 48.4%; Score 661.5; DB 6; Length 285;
Best Local Similarity 49.0%; Pred. No. 3.5e-41;
Matches 146; Conservative 25; Mismatches 66; Indels 61; Gaps 6;
QY 1 MGRAPCCCKKGLKGGPTTPBEDKVLVAHIQRHGHGNRAIPKQAGLLRCCKSCRLRWINY 60
DB 1 MGRAPCCCKKGLKGGPTTPBEDQILVSFILNHGHSNRALPKQAGLLRCCKSCRLRWINY 60
QY 61 LRPDIRKGNFSKEEDTIIHLHELLGNRWSAIAARLPGRTDNEIKVWHTLKKRLDAPA 120
DB 61 LRPDIRKGNFTTKEEDAIISLHQLGNRWSAIAAKLPGRDNEIKVWHTLKKRLLE-DY 119
QY 121 OGGHVAASGGKHKKPKSAKKPAAAAAPASPERSASSVTSSMASSVAEEHGNAGIS 180
DB 120 QPAKPTSNKKGKTKPKS-----ESVITTSNSTRESEELADS-----SNPSGES 163
QY 181 SASASYCAKEESSFTSAEE-----FOIDSPMSET 211
DB 164 LFTSTSPSTSVSSMTLISHGYSNEINMKNKPGDITSTDOECVSFETFGADIDSEFMKET 223
QY 212 LSRPLDGYDVSS-----MEPGDAFVAPPSAD-----DMDYVLGVFMESGEAODL 254
DB 224 LYSODEHNIVYSNDLEVAAGLVEIQOEFQNLGSANNEMI FDESEMDFWFDVLARTGGEODL 281

RESULT 3
US-10-953-349-22502
; Sequence 22502, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 22502
; LENGTH: 275
; TYPE: PRP
; ORGANISM: Glycine max
US-10-953-349-22502

Query Match 48.1%; Score 658; DB 6; Length 275;
Best Local Similarity 46.6%; Pred. No. 6e-41;
Matches 136; Conservative 34; Mismatches 64; Indels 58; Gaps 6;
QY 1 MGRAPCCCKKGLKGGPTTPBEDKVLVAHIQRHGHGNRAIPKQAGLLRCCKSCRLRWINY 60
DB 1 MVRAPCCCKKGLKGGPAPBEDQILTSYIDKHGHNRAIPKQAGLLRCCKSCRLRWINY 60

QY 61 LRPDIRKGNFSKEEDTIIHLHELLGNRWSAIAARLPGRTDNEIKVWHTLKKRLDAPA 120
DB 61 LRPDIRKGNFTTKEEDTIIKLHDMGNRWSAIAAKLPGRDNEIKVWHTLKKRL----- 116
QY 121 OGGHVAASGGKHKKPKSAKKPAAAAAPASPERSASSVTSSMASSVAEEHGNAGIS 180
DB 117 -----LKSQSKSKPSKRAIKP-KIERSDNS-----SITQSEPDWFFNREMD 160
QY 181 SASASYCAKEESSFTSA-----SEFQ-----IDSPWSET----- 211
DB 161 TTSSACTTSSSDFSVTVDGSKNIKSEDTETETPVIDESFWSAAIDETPTWSSSQ 220
QY 212 -----LSMPLDGYDVSMERGAFAVAPPSADMDYVLGVFMESGEAODL 254
DB 221 SLTISNEMRLQYFPANYEETFOQGHAAVYNSNDGDGDFWYDITFRINDSIEL 272

RESULT 4
US-10-953-349-22501
; Sequence 22501, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 22501
; LENGTH: 320
; TYPE: PRP
; ORGANISM: Glycine max
US-10-953-349-22501

Query Match 48.1%; Score 658; DB 6; Length 320;
Best Local Similarity 46.6%; Pred. No. 7.1e-41;
Matches 136; Conservative 34; Mismatches 64; Indels 58; Gaps 6;
QY 1 MGRAPCCCKKGLKGGPTTPBEDKVLVAHIQRHGHGNRAIPKQAGLLRCCKSCRLRWINY 60
DB 46 MVRAPCCCKKGLKGGPAPBEDQILTSYIDKHGHNRAIPKQAGLLRCCKSCRLRWINY 105
QY 61 LRPDIRKGNFSKEEDTIIHLHELLGNRWSAIAARLPGRTDNEIKVWHTLKKRLDAPA 120
DB 106 LRPDIRKGNFTTKEEDTIIKLHDMGNRWSAIAAKLPGRDNEIKVWHTLKKRL----- 161
QY 121 OGGHVAASGGKHKKPKSAKKPAAAAAPASPERSASSVTSSMASSVAEEHGNAGIS 180
DB 162 -----LKSQSKSKPSKRAIKP-KIERSDNS-----SITQSEPDWFFNREMD 205
QY 181 SASASYCAKEESSFTSA-----SEFQ-----IDSPWSET----- 211
DB 206 TTSSACTTSSSDFSVTVDGSKNIKSEDTETETPVIDESFWSAAIDETPTWSSSQ 265
QY 212 -----LSMPLDGYDVSMERGAFAVAPPSADMDYVLGVFMESGEAODL 254
DB 266 SLTISNEMRLQYFPANYEETFOQGHAAVYNSNDGDGDFWYDITFRINDSIEL 317

RESULT 5
US-10-953-349-22503
; Sequence 22503, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252

Query Match	44.3%	Score 606.5	DB 6	length 276
Best Local Similarity	47.4%	Pred. No. 3.2e-37		
Matches 137	Conservative 25	Mismatches 66	Indels 61	Gaps 6
QY	10	MLGKKPWTPEEDKVLVAHIQRHGGNMBALPRQAGLLRCGKSCRLLMNTYLRPDIKGN	69	
Db	1	MGLRKGPTPEEDQILVTSFLLNHGSHNMBALPRQAGLLRCGKSCRLLMNTYLRPDIKGN	60	
QY	70	FSKKEEDTIIHHELLGNRMSAIAARLPRTDNEIGNVHTHLKKRLDPAQGGHVAAGC	129	
Db	61	FTKEEDDAISLHQILGNRMSAIAAKLPRTDNEIGNVHTHLKKLE-DYQAKPRTSN	119	
QY	130	GKKKKKPSAKKPPAAAAAPASPERSASSVTSESMASVAEHNAGISSASAVCAK	189	
Db	120	KKKGRKPPAS-----ESVITSSNSTSESELADS---SNPSSGSLFTSPSTS	163	
QY	190	EESSFTSASEE-----FOIDDSFWSETLSMPLDGYD	220	
Db	164	EVSSTWLLSHQGVNEINMDNKPGRDITDQECVSFETFGADIDEFPMKETTYSQDEHNHY	223	
QY	221	VS-----MEPGDAFVAAPPSAD-----DMDYALGTFMEEGGEQDL	254	

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Qy      1 MGRAPCEMGKCKKPMTPPEEDKLVVAIIORHGNGMRPALPKOAGLLRCGKSCGLRWNTY 60
Db      1 MGRORPCCDKVGKCKKPMPTAEEDQKVAALLTHGHCNRVVKLAGLRCKGKSCGLRWNTY 60
Qy      61 LRPDIKRGNFSKXEEDTIIHLHELGNMWSAIAARLPGRTDNEIKMWNTHLLKKRLDAPA 120
Db      61 LRPDLRKGLLDSEDERLVLDLHAQGNRWSKIAARLPRTDNEIKMWNTHIKKGLRKM 120
Qy      121 OGCHVAASGGKHKHKPKAKKRAAAAAAPPSPPERSASSSVTESMSSVAEEH-----G 175
Db      121 ----IDPVTHQLEPRPPRRPQDATTPRPPPEQIEESEEEQESPPLPEHETAPP 176
Qy      176 NGISASASVACKEESSF-----TSASEEFOIDDSFWSETLSM-PLDG----- 218
Db      177 PAAAAEAATSNCSVSPASVLSBSCSSASASAANDVAEMPEPMTFGMDGIMDVGNGLI 236
Qy      219 -----YDSMEPGDAFVAAPPSADMDMYL 242
Db      237 SGAGVDVDVDVDPFDHYHNDASFDDQDVM 266

RESULT 8
US-10-449-902-39724
; Sequence 39724, Application US/10449902
; Publication No. US20060123505A1
GENERAL INFORMATION:
APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SOFTWARE: PatentIn Ver. 2.11
SEQ ID NO 39724

```

LENGTH: 300
TYPE: PRT
ORGANISM: Oryza sativa
US-10-449-902-39724

Query Match
Best Local Similarity 45.7%; Pred. No. 1.2e-32;
Matches 118; Conservative 38; Mismatches 66; Indels 36; Gaps 6;

QY 1 MGRAPCCCKMGLKKGWTPBEDKVLVAHIQRHGHGNWRALPKOAGLLRCGKSCRLRWNY 60
DB 1 MGRAPCCCKMGLKKGWTPBEDKVLVAHIQRHGHGNWRALPKOAGLLRCGKSCRLRWNY 60
QY 61 LRPDIRKGNFSKEEDTIIHLHLLGNRWSAIAARLPGRDNEIKVWHTLKKRLDA-- 115
DB 61 LRPDIRKGNFSKEEDTIIHLHLLGNRWSAIAARLPGRDNEIKVWHTLKKRLDA-- 115
QY 116 LQAPAGGVAAAGSGKKHKKPKAPAAAAPASPERSASSVTSSMASSVAEEHG 175
DB 121 LDDPPPGPAAAGCPAAAHMAQWETARLEAEARLSLSSGVAATTTTAAATTTTSSASSST 180
QY 176 NAGISSASAVCAKESSFTSASEF-----QIDDSFWSETLSMPLDGYVMEGDAP 229
DB 181 TAGPVAAAA-----TSPADVFLRLWNSSTIGDSF--RKLAVVAAG---SSSPSRAD 225
QY 230 V-----APPSAD 237
DB 226 VTKDAVKQEBEAPAGDD 243

RESULT 9
US-10-449-902-34326
Sequence 34326; Application US/10449902
Publication No. US20060123505A1
GENERAL INFORMATION:
APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
TITLE OF INVENTION: Foundation for Advancement of International Science.
FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 34326
LENGTH: 266
TYPE: PRT
ORGANISM: Oryza sativa
US-10-449-902-34326

Query Match
Best Local Similarity 42.5%; Pred. No. 2.9e-31;
Matches 113; Conservative 31; Mismatches 50; Indels 72; Gaps 7;

QY 1 MGRAPCCCKMGLKKGWTPBEDKVLVAHIQRHGHGNWRALPKOAGLLRCGKSCRLRWNY 60
DB 1 MGRAPCCCKMGLKKGWTPBEDKVLVAHIQRHGHGNWRALPKOAGLLRCGKSCRLRWNY 60
QY 61 LRPDIRKGNFSKEEDTIIHLHLLGNRWSAIAARLPGRDNEIKVWHTLKKRLDA-- 118
DB 61 LRPDIRKGNFSKEEDTIIHLHLLGNRWSAIAARLPGRDNEIKVWHTLKKRLDA-- 118
QY 119 LQAPAGGVAAAGSGKKHKKPKAPAAAAPASPERSASSVTSSMASSVAEEHG 175
DB 121 LQAPAGGVAAAGSGKKHKKPKAPAAAAPASPERSASSVTSSMASSVAEEHG 175
QY 139 AKPPAAAAAPASPERSASSVTSSMASSVAEEHG 175
DB 139 AKPPAAAAAPASPERSASSVTSSMASSVAEEHG 175

DB 181 ISSASAS-----VCAKESSFTSAS 198
QY 179 ISSASAS-----VCAKESSFTSAS 198
DB 237 GSSASSSSSPPATASSRAFTFANAS 262

RESULT 10
US-10-953-349-33714

Sequence 33714; Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nikolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 33714
LENGTH: 331
TYPE: PRT
ORGANISM: Zea mays subsp. mays
FEATURE:
NAME/KEY: misc feature
LOCATION: (204)..(204)
OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-10-953-349-33714

Query Match
Best Local Similarity 36.9%; Pred. No. 4.4e-31;
Matches 124; Conservative 34; Mismatches 68; Indels 110; Gaps 10;

QY 1 MGRAPCCCKMGLKKGWTPBEDKVLVAHIQRHGHGNWRALPKOAGLLRCGKSCRLRWNY 59
DB 1 MGRAPCCCKMGLKKGWTPBEDKVLVAHIQRHGHGNWRALPKOAGLLRCGKSCRLRWNY 59
QY 60 YLRPDIRKGNFSKEEDTIIHLHLLGNRWSAIAARLPGRDNEIKVWHTLKKRLDA-- 116
DB 60 YLRPDIRKGNFSKEEDTIIHLHLLGNRWSAIAARLPGRDNEIKVWHTLKKRLDA-- 116
QY 117 LQAPAGGVAAAGSGKKHKKPKAPAAAAPASPERSASSVTSSMASSVAEEHG 175
DB 121 LQAPAGGVAAAGSGKKHKKPKAPAAAAPASPERSASSVTSSMASSVAEEHG 175
QY 146 AAPAPASP-----ERSASSVTSSMASSVAEEHG 175
DB 181 SPPPPPGPAPAFSGLESPTSTXSPSEVLFPASAAHDTHAULTSRAVAEAFGAEOQORPA 240
QY 176 NAGI-----SSASAVCAKESSFTSASEFQIDDSFW 208
DB 241 DTRAAAADAPFLAGVLLGCSVAGAEKGFPAASSTDAVLPAPATA 327
QY 209 SETLSWPLDGY-----DVSMEGDAFVAPPSA 235
DB 292 SSLNWNVNSMSSSTSLTSDAVTDPAALVLPAPATA 327

RESULT 11
US-10-449-902-29589
Sequence 29589; Application US/10449902
Publication No. US20060123505A1
GENERAL INFORMATION:
APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
TITLE OF INVENTION: Foundation for Advancement of International Science.
FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: JP 2002-203269

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? PRIOR FILING DATE: 2002-05-30
? PRIOR APPLICATION NUMBER: JP 2002-383870
? PRIOR FILING DATE: 2002-12-11
? NUMBER OF SEQ ID NOS: 56791
? SOFTWARE: Patentin Ver. 2.1
? SEQ ID NO 29589
? LENGTH: 260
? TYPE: prt
? ORGANISM: Oryza sativa
US-10-449-902-29589

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Query Match	37.4%	Score 511;	DB 6;	Length 260;
Best Local Similarity	52.1%;	Pred. No. 2.5e-30;		
Matches 100;	Conservative 22;	Mismatches 50;	Indels 20;	Gaps 2;

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QY      1  MGRAPCECEMGIKJGKWTETEEEDKVLVAH IORHGHGMWRAIPKQAGLLRCKSKSRLRYIN  60
Dh      1  MGRSPCCEBAHNNKGMWTKTEEDORLIAYIRAHOGCMRSLPKAAGLLRCKSKSRLRYMNY  60
QY      61  LRPIDKRGNFYSKEEDDTIHLHELLGNRWSAIPARLPGRTDNEIKVMVHTHLKKRIDAP-  119
Dh      61  LRPIDKRGNFDTODEDELIIRLHSLLGNNKMSLIGOLPGRTDNEIKVMVNTHIKRLLIARG  120
QY      120  -----AOGGHVAAAGGKHKHKPKAKKPAALAAA-----PASPEBRASSS  160
Dh      121  IDPQTHRPULLSGGDGIIAASNKAAPPPHPISVPAKAAAAAIIFAVAKPPPPRPVDSDDG  180
QY      161  VTSSMASSVAE  172
Dh      181  CRSSGTTSTGE  192

```

RESULT 12
US-10-449-902-44757
; Sequence 44757, Application US/10449902
; Publication No. US20060123505A1

```

1  APPLICANT: National Institute of Agrobiological Sciences.
2  APPLICANT: Bio-oriented Technology Research Advancement Institution.
3  APPLICANT: The Institute of Physical and Chemical Research.
4  APPLICANT: Foundation for Advancement of International Science.
5  TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
6  FILE REFERENCE: MOA-A0205Y1-US/10/449,902
7  CURRENT FILING DATE: 2003-05-29
8  PRIOR APPLICATION NUMBER: JP 2002-209269
9  PRIOR FILING DATE: 2002-05-30
10 PRIOR APPLICATION NUMBER: JP 2002-383870
11 PRIOR FILING DATE: 2002-12-11
12 NUMBER OF SEQ ID NOS: 56791
13 SOFTWARE: Patentin Ver. 2.1
14 SEQ ID NO 44757
15 LENGTH: 260
16 TYPE: PRT
17 ORGANISM: Oryza sativa
18 OS-10-449-902-44757

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Query Match	37.4%	Score 511;	DB 6;	Length 260;
Best Local Similarity	52.1%;	Pred. No. 2.5e-30;		
Matches 100;	Conservative 22;	Mismatches 50;	Indels 20;	Gaps 2

[illegible]

QY	161	VTESSMASSVAE	172
Db	181	CRSSSGTTSTGE	192

RESULT 13
US-10-449-902-47791
; Sequence 47791, Application US/10449902
; Publication No. US20060123505A1

APPLICANT: National Institute of Agrobiological Sciences.
 APPLICANT: Bio-oriented Technology Research Advancement Institution
 APPLICANT: The Institute of Physical and Chemical Research.
 APPLICANT: Foundation for Advancement of International Science.
 TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
 FILE REFERENCE: MOA-A0205Y1-US
 CURRENT APPLICATION NUMBER: US/10/449,902
 CURRENT FILING DATE: 2003-05-29
 PRIOR APPLICATION NUMBER: JP 2002-203269
 PRIOR FILING DATE: 2002-05-30
 PRIOR APPLICATION NUMBER: JP 2002-383870
 PRIOR FILING DATE: 2002-12-11
 NUMBER OF SEQ ID NOS: 56791
 SOFTWARE: Patentin Ver. 2.1
 SEQ ID NO 47791
 LENGTH: 260
 TYPE: PRT
 ORGANISM: *Oryza sativa*
 OS-10-449-902-47791

Query Match	37.4%	Score 511	DB 6	Length 260
Best Local Similarity	52.1%	Pred. No. 2.5e-30		
Matches 100; Conservative	22	Mismatches 50	Indels 20	Gaps 2

[illegible]

RESULT 14
US-10-449-902-32367
; Sequence 32367, Application US/10449902
; Publication No. US20060123505A1

APPLICANT: National Institute of Agrobiological Sciences.
 APPLICANT: Bio-oriented Technology Research Advancement Institution.
 APPLICANT: The Institute of Physical and Chemical Research.
 APPLICANT: Foundation for Advancement of International Science.
 TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
 FILE REFERENCE: MOA-A0205Y1-US
 CURRENT APPLICATION NUMBER: US/10/449,902
 CURRENT FILING DATE: 2003-05-29
 PRIOR APPLICATION NUMBER: JP 2002-203269
 PRIOR FILING DATE: 2002-05-30
 PRIOR APPLICATION NUMBER: JP 2002-363870
 PRIOR FILING DATE: 2002-12-11
 NUMBER OF SEQ ID NOS: 56791
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 32367
 LENGTH: 311
 TYPE: PRT

ORGANISM: *Oryza sativa*
US-10-449-902-32367

Query Match	37.1%;	Score 507.5;	DB 6;	Length 311;
Best Local Similarity	43.7%;	Pred. No. 5.4e-30;		
Matches 111;	Conservative 34;	Mismatches 72;	Indels 37;	Gaps 6;

[illegible]

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RESULT 15
US-10-953-349-10216
: Sequence 10216, Application US/10953349
: Publication No. US20060107345A1
: GENERAL INFORMATION:
: APPLICANT: ALEXANDROV, Nikolaï et al.
: TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
: TITLE OF INVENTION: ENCODED THERBY
: FILE REFERENCE: 2750-1579PUS2
: CURRENT APPLICATION NUMBER: US/10/953,349
: CURRENT FILING DATE: 2004-09-30
: NUMBER OF SEQ ID NOS: 40252
: SOFTWARE: PatentIn version 3.3
: SEQ ID NO 10216
: LENGTH: 342
: TYPE: PRT
: ORGANISM: Arabidopsis thaliana
US-10-953-349-10216

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Query Match	36.7%	Score 502.5;	DB 6;	Length 342;
Best Local Similarity	43.3%;	Pred. No. 1.4e-29;		
Matches 104;	Conservative 34;	Mismatches 59;	Indels 43;	Gaps 5

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Qy 1 GGRAPCCCEMGLKGGWPFEEEDVVAH1ORHGHGMWPLPKOAGLLRGCSKSLRLINy 60
Db 1 GGRAPCCCEITGKRGKWTAEEDITLKY1QIOTNEGSSRLSPKAGLLRGCSKSLRLINy 60
Qy 61 LRPDIKRGFNSKEEDTIIHLHELLGNRSASIAARPGRTDNEIKVWMTHLKRL---D 117
Db 61 LRRDLKRGNTSDEEBEIIYKLSHLGNRSLSIATHLPGRTDNEIIKYWMTSHLRKIYAF 120
Qy 118 APAQGGH-----VAASGGKKHKKPKPSAKKPPAAAAAAPPSPRSASSVTES 164
Db 121 AVSGGHHNLVNDVVLKKSCESSSGAKNNNTKTKKKK-----GRTSRSSMKKH 168
Qy 165 SMASSVAEHHGNAGISASASVCAKEESSFTASSEEQIDDSFWSEITLWMLGYDVSME 224
Db 169 K-----QMTVASQCFOSPKELESFSGGGNGNGNEBSLG-PYMLDDELE 213

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Search completed: June 24, 2006, 00:09:11
Job time : 23 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 24, 2006, 00:04:07 ; Search time 50 Seconds

(without alignments)
449,907 Million cell updates/sec

Title: US-10-521-811-2

Perfect score: 1368
Sequence: 1 MBRAPCEKMGKKGFWTPE.....MDYWLGVFMESEGAQDLPOI 257

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents AA:*
1: /EMC_Celerra_SIDS3/ProdData/2/1aa/5_COMB.pep:*
2: /EMC_Celerra_SIDS3/ProdData/2/1aa/6_COMB.pep:*
3: /EMC_Celerra_SIDS3/ProdData/2/1aa/7_COMB.pep:*
4: /EMC_Celerra_SIDS3/ProdData/2/1aa/H_COMB.pep:*
5: /EMC_Celerra_SIDS3/ProdData/2/1aa/PCITUS_COMB.pep:*
6: /EMC_Celerra_SIDS3/ProdData/2/1aa/RE_COMB.pep:*
7: /EMC_Celerra_SIDS3/ProdData/2/1aa/backfill1es1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	669.5	48.9	278	1 US-08-722-626B-2	Sequence 2, Appl
2	640	46.8	273	2 US-09-533-029-62	Sequence 62, Appl
3	582	42.5	122	2 US-09-533-029-112	Sequence 112, Appl
4	548	40.1	159	2 US-09-640-211A-2161	Sequence 2161, Appl
5	547.5	40.0	146	2 US-09-640-211A-1110	Sequence 1110, Appl
6	522.5	38.2	412	2 US-09-640-211A-2258	Sequence 2258, Appl
7	506.5	37.0	327	2 US-09-533-029-68	Sequence 68, Appl
8	502	36.7	391	2 US-09-640-211A-2259	Sequence 2259, Appl
9	487	36.3	294	2 US-09-453-387A-2	Sequence 2, Appl
10	495.5	36.2	225	2 US-09-640-211A-2277	Sequence 2277, Appl
11	495	36.0	255	2 US-09-640-211A-2261	Sequence 2261, Appl
12	493	35.8	146	2 US-09-640-211A-2110	Sequence 2110, Appl
13	490	35.7	302	2 US-09-640-211A-2201	Sequence 2201, Appl
14	488.5	35.7	171	2 US-09-453-387A-6	Sequence 6, Appl
15	487	35.6	102	2 US-09-640-211A-872	Sequence 872, Appl
16	483	35.3	176	2 US-09-640-211A-2238	Sequence 2238, Appl
17	483	35.3	371	2 US-09-533-029-86	Sequence 86, Appl
18	481	35.2	269	2 US-09-533-029-94	Sequence 94, Appl
19	476	34.8	144	2 US-09-640-211A-2260	Sequence 2260, Appl
20	475	34.7	205	2 US-09-640-211A-2248	Sequence 2248, Appl
21	471.5	34.5	148	2 US-09-640-211A-1093	Sequence 1093, Appl
22	470	34.4	139	2 US-09-640-211A-1085	Sequence 1085, Appl
23	469.5	34.3	336	2 US-09-533-029-58	Sequence 58, Appl
24	465.5	34.0	192	2 US-09-640-211A-2210	Sequence 2210, Appl
25	465	34.0	414	2 US-09-640-211A-2247	Sequence 2247, Appl
26	463	33.8	153	2 US-09-640-211A-2194	Sequence 2194, Appl

27	459.5	33.6	226	2 US-09-640-211A-2256	Sequence 2256, Appl
28	459	33.6	226	2 US-09-453-387A-4	Sequence 4, Appl
29	456	33.3	126	2 US-09-640-211A-2139	Sequence 2139, Appl
30	450	32.9	107	2 US-09-640-211A-2156	Sequence 2156, Appl
31	450	32.9	107	2 US-09-640-211A-2244	Sequence 2244, Appl
32	449	32.8	107	2 US-09-640-211A-2230	Sequence 2230, Appl
33	445	32.5	113	2 US-09-640-211A-1099	Sequence 1099, Appl
34	440.5	32.2	119	2 US-09-640-211A-1082	Sequence 1082, Appl
35	438	32.0	109	2 US-09-640-211A-2141	Sequence 2141, Appl
36	427	31.2	128	2 US-09-640-211A-1083	Sequence 1083, Appl
37	427	31.2	146	2 US-09-640-211A-2115	Sequence 2115, Appl
38	413.5	30.2	175	2 US-09-640-211A-2159	Sequence 2159, Appl
39	408	29.8	112	2 US-09-640-211A-1112	Sequence 1112, Appl
40	404	29.5	101	2 US-09-640-211A-2169	Sequence 2169, Appl
41	398	29.1	107	2 US-09-640-211A-1118	Sequence 1118, Appl
42	390.5	28.5	208	2 US-09-640-211A-2250	Sequence 2250, Appl
43	390	28.5	148	2 US-09-640-211A-2206	Sequence 2206, Appl
44	387.5	28.3	168	2 US-09-640-211A-2245	Sequence 2245, Appl
45	381	27.9	224	2 US-09-640-211A-919	Sequence 919, Appl

ALIGNMENTS

RESULT 1
US-08-722-626B-2
Sequence 2, Application US/08722626B
Patent No. 5939601
GENERAL INFORMATION:
APPLICANT: Yang, Yimong
TITLE OF INVENTION: Novel Genes Associated With Enhanced
Disease Resistance In Plants
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESSES:
ADDRESSER: Dann, Dorfman, Herrell and Skillman
STREET: 1601 Market Street Suite 720
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103-2307
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/722,626B
FILING DATE: 27-SEP-1996
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Pat Hagan
REGISTRATION NUMBER: 27,643
REFERENCE/DOCKET NUMBER: 97-0010
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215 563-4100
TELEFAX: 215 563-4044
TELEX:
INFORMATION FOR SEQ. ID NO. 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 278 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: Internal
ORIGINAL SOURCE:
US-08-722-626B-2


```

Query Match      48.9%; Score 669.5; DB 1; Length 278;
Best Local Similarity 47.2%; Pred. No.4.2e-61;
Matches 141; Conservative 37; Mismatches 56; Indels 65; Gaps 10.

QY      1 MGRAPCCCKMKGLKKGPWTPEEDKVLVAHIORHGHGNMPLPKQAGILRCGKSCRRLRWNY 60
Db      1 MVRAPCCCKMKGLKKGPWTPEEDQILISITQNGHGNMPLAPQAGILRCGKSCRRLRWNY 60

QY      61 LRPIIKRGNFESKEEDTIIHLHELLGNFWSAIAARLPGRTDNEIKNWHTHKRLD--A 118
Db      61 LRPIIKRGNFTEEBEETIIQLHEMLGNFWSAIAAALPGRTDNEIKNWHTHKRLDKDYK 120

QY      119 PAQGHVAASGQKKKKPKPS--AKKPAAAA-----APASPERSASSS 160
Db      121 PPQ-----NSKRSKSKNHDSDKPTTSSESNNSDLTINTQKHIDSPVLAPNSPQISS 173

QY      161 VTSSMASSVAEBHGNAGISSASAVCAKEESSFTSASEEF-QIDDSFWSSETLS----- 213
Db      174 STEMSTVTLV-DDH-----QNVVVKQE--VNESESEYFEIDESFWTDELTTDNMNS 221

QY      214 -----MPLGDYDVSMEGDAFVAPPSADDMDYIIGVMESEGAODLPQ 256
Db      222 STDHVMVAANOELQVLPFSSSF--KEENVDIATKMDMDMFYWNVFIKTDIDPELPE 277

RESULT 2
US-09-533-029-62
; Sequence 62, Application US/09533029
; Patent No. 6664446
; GENERAL INFORMATION:
; APPLICANT: Heard, Jacqueline
; APPLICANT: Brown, Pierre
; APPLICANT: Riechmann, Jose-Luis
; APPLICANT: Keddie, James
; APPLICANT: Pineda, Omaira
; APPLICANT: Adam, Luc
; APPLICANT: Samaha, Raymond
; APPLICANT: Zhang, James
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ratcliffe, Oliver
; APPLICANT: Pilgrim, Marsha
; APPLICANT: Jiang, Cai-Zhong
; APPLICANT: Reuber, Lynne
; TITLE OF INVENTION: DISEASE-INDUCED POLYNUCLEOTIDES
; FILE REFERENCE: MBI-010
; CURRENT APPLICATION NUMBER: US/09/533.029
; CURRENT FILING DATE: 2000-03-22
; EARLIER APPLICATION NUMBER: 60/125, 814
; EARLIER FILING DATE: 1999-03-23
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 62
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; OTHER INFORMATION: G233
; US-09-533-029-62

```

	Query Match	46.8%	Score 640;	DB 2;	Length 273;
	Best Local Similarity	54.8%;	Pred. No. 4,8e-58;		
	Matches 132,	Conservative 19;	Mismatches 44;	Indels 46;	Gaps 4
Oy	1	MGRAPCCCKMGKKGPMTPPEEDKVVAHIORHGHNWMLPKQAGILRCGSKSCRLLRWNY	60		
Dd	1	MGRAPCCCKMGKKGPMTPPEEDQIVLVSFLNGHSNMRLPQOAGILRCGSKCRIRMWNY	60		
Oy	61	LRPDIKGNFNSKEEEDTIIHLHELGNWSAIAARLPGETDNEIGNVHTHLKKGLDAPA	120		
Dd	61	LKPDIKGNFTKEEDDAIISLHQILGNRKSAAALPTGTDEIGNVHTHLKKGLE-DY	119		
Oy	121	QGHHVASGGKHKKPKSAKRPAALAAPASPERSSASSVTSESMASVAEEHGNAGIS	180		

Db		120 QPAPKTSNKKKGTRKPS-----ESVITSSNSTRSESELADS---- <td>163</td>	163
Qy	181 SASASVCAKESSESFTSASEE-----FOIDGSFWSET	211	
Db	164 LFTSPSTSEVSMTLLSHDGYSEINMNDNRPGDISTIDECVSEFTFGADIDESFWKET	223	
Qy	212 L 212		
Db	224 L 224		
 RESULT 3 US-09-533-029-112 Sequence 112 Application US/09533029 Patent No. 6664446 GENERAL INFORMATION: APPLICANT: Heard, Jacqueline APPLICANT: Broun, Pierre APPLICANT: Riechmann, Jose-Luis APPLICANT: Keddie, James APPLICANT: Pineda, Omaira APPLICANT: Adam, Luc APPLICANT: Samaha, Raymond APPLICANT: Zhang, James APPLICANT: Yu, Guo-Liang APPLICANT: Ratcliffe, Oliver APPLICANT: Pilgrim, Marsha APPLICANT: Jiang, Cai-Zhong APPLICANT: Reuter, Lynne TITLE OF INVENTION: DISEASE-INDUCED POLYNUCLEOTIDES FILE REFERENCE: MB1-010 CURRENT APPLICATION NUMBER: US/09/533,029 CURRENT FILING DATE: 2000-03-22 EARLIER APPLICATION NUMBER: 60/125,814 EARLIER FILING DATE: 1999-03-23 NUMBER OF SEQ ID NOS: 121 SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 112 LENGTH: 122 TYPE: prt ORGANISM: Arabidopsis thaliana FEATURE: OTHER INFORMATION: G241 US-09-533-029-112			

```

Query March 42.5%; Score 582; DB 2; Length 122;
Best Local Similarity 85.5%; Pred. No. 1,5e-52;
Matches 100; Conservative 11; Mismatches 6; Indels 0; Gaps 0

Dy 1 MGRAPCCCKMGLKKGPWTPEEDKVLVAHIORHGNMRLPRQAGILRGSKCRLRWNY 60
1 MGRAPCCCKMGLKKGPWTPEEDQILVSIPLNHGHSNMLPRQAGILRGSKCRLRWNY 60

Dy 61 LRPDIKRGNSKEEDDTIHLHELLGNWSAIAALPGRTDNEIKVWHTHLKKRLD 117
61 LKPIIKRGNTPEEDDAIISLHQILGNWSAIAALPGRTDNEIKVWHTHLKKRLD 117

RESULT 4
US-09-640-211A-2161
; Sequence 2161, Application US/09640211A
; Patent No. 6833446
; GENERAL INFORMATION:
; APPLICANT: Wood, Marion
; APPLICANT: Shenk, Michael A.
; APPLICANT: McGrath, Anneete
; APPLICANT: Glenn, Matthew
; TITLE OF INVENTION: Compositions and Methods for the
; FILE REFERENCE: 11000.1021C1U
; CURRENT APPLICATION NUMBER: US/09/640,211A
; CURRENT FILING DATE: 2000-08-16

```


[illegible]

```

RESULT 8
US-09-640-211A-2259
: Sequence 2259, Application US/09640211A
: Patent No. 6833446
: GENERAL INFORMATION:
: APPLICANT: Wood, Marion
: APPLICANT: Shenk, Michael A.
: APPLICANT: McGrath, Annette
: APPLICANT: Glenn, Matthew
: TITLE OF INVENTION: Compositions and Methods for the
: TITLE OF INVENTION: Modification of Gene Transcription
: FILE REFERENCE: 11000.1021CIU
: CURRENT APPLICATION NUMBER: US/09/640,211A
: CURRENT FILING DATE: 2000-08-16
: NUMBER OF SEQ ID NOS: 2368
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 2259
: LENGTH: 391
: TYPE: prt
: ORGANISM: Pinus radiata
: US-09-640-211A-2259

```

Query Match	36.7%;	Score 502;	DB 2;	Length 391;
Best Local Similarity	41.9%;	Pred. No. 1.8e-43;		
Matches 108; Conservative	30;	Mismatches 84;	Indels 36;	Gaps 6

```

RESULT 9
US-09-453-387A-2
: Sequence 2, Application US/09453387A
: Patent No. 6828476
: GENERAL INFORMATION:
: APPLICANT: Wilkins, Thea A.
: APPLICANT: The Regents of the University of California
: TITLE OF INVENTION: Cotton Transcription Factors and Their Uses
: FILE REFERENCE: 023070-095600US
: CURRENT APPLICATION NUMBER: US/09/453.387A
: CURRENT FILING DATE: 1999-12-02
: NUMBER OF SEQ ID NOS: 26
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 2
: LENGTH: 294
: TYPE: PRT
: ORGANISM: Gossypium hirsutum
: US-09-453-387A-2

```

Query Match	36.3%;	Score 497;	DB 2;	Length 294;
Best Local Similarity	43.3%;	Pred. No. 3.9e-43;		
Matches 104; Conservative	43;	Mismatches 77;	Indels 16;	Gaps 4;

```
QY      181 SASASVCAKEESSTTSAS-----EEFQIDDSFMWSTLSMLDGYDVXSMEPGDAFYAPPSA    235  
       :: : || : :: | ||| : :||:::|| :  
Db     172 QPKSNTDSLSEPNCTASSGGTTDEEQ--EQLHKKQQYGPGNGDPINLEISIGIVSDSS   229
```

```

RESULT 10.
US-09-640-211A-2277
: Sequence 2277, Application US/09640211A
: Patent No. 6833446
:
GENERAL INFORMATION:
APPLICANT: Wood, Marion
APPLICANT: Shenk, Michael A.
APPLICANT: McGrath, Annette
APPLICANT: Glenn, Matthew
:
TITLE OF INVENTION: Compositions and Methods for the
:
TITLE OF INVENTION: Modification of Gene Transcription
:
FILE REFERENCE: 11000.1021CIU
:
CURRENT APPLICATION NUMBER: US/09/640.211A
:
CURRENT FILING DATE: 2000-08-16
:
NUMBER OF SEQ ID NOS: 2368
:
SOFTWARE: FastSeq For Windows Version 4.0
:
SEQ ID NO 2277
:
LENGTH: 225
:
TYPE: PR1
:
ORGANISM: Pinus radiata
:
US-09-640-211A-2277

```

Query Match	36.2%	Score 495.5;	DB 2;	Length 225;
Best Local Similarity	50.5%	Pred. No. 3.7e-43;		
Matches 97;	Conservative 27;	Mismatches 51;	Indels 17;	Gaps 4;

QY 169 SVAEHEGNAGIS 180
| ||| : :
DB 176 SPAEHPDLNLN 187

RESULT 11
US-09-640-211A-2261
Sequence 2261, Application US/09640211A
Patent No. 6833446
GENERAL INFORMATION:
APPLICANT: Wood, Marion
APPLICANT: Shenk, Michael A.
APPLICANT: McGrath, Annette

```

; APPLICANT: Glenn, Matthew
; TITLE OF INVENTION: Compositions and Methods for the
; FILE REFERENCE: 11000.1021CIU
; CURRENT APPLICATION NUMBER: US/09/640,211A
; CURRENT FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 2368
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2261
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Pinus radiata
US-09-640-211A-2261
```

```

Query Match          36.2%; Score 495; DB 2; Length 255;
Best Local Similarity 46.0%; Pred. No. 5.1e-43;
Matches 103; Conservative 28; Mismatches 65; Indels 28; Gaps 3;
```

```

QY 1 MGRAPCCCKMGLKGPWTPPEEDKVLVAHIQRHGHGWMRALPKOAGLLRCGSKRLRWINY 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 1 MGRSPCCCKMNTKMGATKEEDRLIAHRTGEGCRSLPKAAGLLRCGSKRLRWINY 60
QY 61 LRPDIRKGNFSKEEDTIIHLHELGNRWSAIAARLPGRDNEIKVWHTLKKRLDAPA 120
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 61 LRDLKRGNFSEDEDELIVIKLHSLGNKWSLIGRLPGRTDNEIKVWHTHIKRLINRG 120
QY 121 OGGHVAASGGKHKKKPKSA-----KKPAAAAAPPASPERASASSVTSSMA 167
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 121 LDPQSHRPLQPHNSNTTCSPLPALHEHELVPQRPTPEIADPFQYERSESSPMEPAT-- 178
QY 168 SSVAEEHGNAGI-----SSASASVCAKESSFTSAS 198
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 179 SKDAEHPDLNLDLCISLPVHSPPTASSVDGTVDGSKNSVS 222
```

```

RESULT 12
US-09-640-211A-2110
; Sequence 2110, Application US/09640211A
; Patent No. 6833446
; GENERAL INFORMATION:
; APPLICANT: Wood, Marion
; APPLICANT: Shenk, Michael A.
; APPLICANT: McGrath, Annette
; APPLICANT: Glenn, Matthew
; TITLE OF INVENTION: Compositions and Methods for the
; FILE REFERENCE: 11000.1021CIU
; CURRENT APPLICATION NUMBER: US/09/640,211A
; CURRENT FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 2368
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2110
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Eucalyptus grandis
US-09-640-211A-2110
```

```

Query Match          36.0%; Score 493; DB 2; Length 146;
Best Local Similarity 64.1%; Pred. No. 3.6e-43;
Matches 93; Conservative 14; Mismatches 24; Indels 14; Gaps 2;
```

```

QY 6 CCEKMGGLKGPWTPPEEDKVLVAHIQRHGHGWMRALPKOAGLLRCGSKRLRWINYLRPD 65
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 1 CCEKMGGLKGPWTPPEEDKVLVAHIQRHGHGWMRALPKOAGLLRCGSKRLRWINYLRPD 60
QY 66 KRGNFSKEEDTIIHLHELGNRWSAIAARLPGRDNEIKVWHTLKKRLDAPA 116
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 61 KRGNFSKEEDTIIHLHELGNRWSAIAARLPGRDNEIKVWHTLKKRLDAPA 120
QY 117 DAPAGHVAASGGKHKKKPKSAKK 141
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 121 HKPKNDALVSSDG-----OSKSAK 140
```

```

RESULT 13
US-09-640-211A-2201
; Sequence 2201, Application US/09640211A
; Patent No. 6833446
; GENERAL INFORMATION:
; APPLICANT: Wood, Marion
; APPLICANT: Shenk, Michael A.
; APPLICANT: McGrath, Annette
; APPLICANT: Glenn, Matthew
; TITLE OF INVENTION: Compositions and Methods for the
; FILE REFERENCE: 11000.1021CIU
; CURRENT APPLICATION NUMBER: US/09/640,211A
; CURRENT FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 2368
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2201
; LENGTH: 171
; TYPE: PRT
; ORGANISM: Eucalyptus grandis
US-09-640-211A-2201
```

```

Query Match          35.8%; Score 490; DB 2; Length 171;
Best Local Similarity 72.0%; Pred. No. 9.2e-43;
Matches 85; Conservative 16; Mismatches 17; Indels 0; Gaps 0;
```

```

QY 1 MGRAPCCCKMGLKGPWTPPEEDKVLVAHIQRHGHGWMRALPKOAGLLRCGSKRLRWINY 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 1 MGRSPCCCKMNTKMGATKEEDRLIAHRTGEGCRSLPKAAGLLRCGSKRLRWINY 60
QY 61 LRPDIRKGNFSKEEDTIIHLHELGNRWSAIAARLPGRDNEIKVWHTLKKRLDAPA 118
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 61 LRDLKRGNFSEDEDELIVIKLHSLGNKWSLIGRLPGRTDNEIKVWHTHIKRLDAPA 118
```

```

RESULT 14
US-09-453-387A-6
; Sequence 6, Application US/09453387A
; Patent No. 6828476
; GENERAL INFORMATION:
; APPLICANT: Wilkins, Thea A.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Cotton Transcription Factors and Their Uses
; FILE REFERENCE: 023070-095600US
; CURRENT APPLICATION NUMBER: US/09/453,387A
; CURRENT FILING DATE: 1999-12-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 302
; TYPE: PRT
; ORGANISM: Gossypium hirsutum
US-09-453-387A-6
```

```

Query Match          35.7%; Score 488.5; DB 2; Length 302;
Best Local Similarity 41.3%; Pred. No. 3.1e-42;
Matches 112; Conservative 38; Mismatches 84; Indels 37; Gaps 8;
```

```

QY 1 MGRAPCCCKMGLKGPWTPPEEDKVLVAHIQRHGHGWMRALPKOAGLLRCGSKRLRWINY 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 1 MGRSPCCCKMNTKMGATKEEDRLIAHRTGEGCRSLPKAAGLLRCGSKRLRWINY 60
QY 61 LRPDIRKGNFSKEEDTIIHLHELGNRWSAIAARLPGRDNEIKVWHTLKKRLDAPA 120
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 61 LRDLKRGNFSEDEDELIVIKLHSLGNKWSLIGRLPGRTDNEIKVWHTHIKRLDAPA 119
QY 121 OGGHVAASGGKHKKKPKSAKKPAAAAAPPASPERASASSVTSSMA----- 167
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 120 QSSPAAPS-----KNPEAARGRGAGNTNGSGSSSTHVTRATRCSTKVFINPHT 174
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 168 -----SSVAEEHGN-----AGISSASASVCAKESSFTS--ASEEFOJIDDSFWESETLS- 213
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
```

Db 175 QNRDPKRSSTCSNHGDRREPKTMNELLLPIMSESENEGTTDHISSDFTDFNMGEFCLSD 234

QY 214 -MPLDGYDVS-MEPGDAFVAFPSADD-MDY 240

Db 235 LINSDFCDVNEIYNNGFDSFSPDQPMDF 265

RESULT 15

US-09-640-211A-872

; Sequence 872, Application US/09640211A

; Patent No. 6833446

; GENERAL INFORMATION:

; APPLICANT: Wood, Marion

; APPLICANT: Shenk, Michael A.

; APPLICANT: McGrath, Annette

; APPLICANT: Glenn, Matthew

; TITLE OF INVENTION: Compositions and Methods for the

; FILE REFERENCE: 11000.1021CIU

; CURRENT APPLICATION NUMBER: US/09/640,211A

; CURRENT FILING DATE: 2000-08-16

; NUMBER OF SEQ ID NOS: 2368

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 872

; LENGTH: 102

; TYPE: PRT

; ORGANISM: Eucalyptus grandis

US-09-640-211A-872

Query Match 35.6%; Score 487; DB 2; Length 102;
Best Local Similarity 79.4%; Pred. No. 8.8e-43;
Matches 81; Conservative 13; Mismatches 8; Indels 0; Gaps 0;

QY 1 MGRAPCCCEKMGKGPWTPEEDKYV/AHIOHGHGHWRALPKQAGLLRCGKSCRLRWINY 60

Db 1 MARTPCCEKMGKGPWTPEEDQILSHIQFGHSNWRALPRQAGLLRCGKSCRLRWINY 60

QY 61 LRPDIKRGNFSKEEDTITHELGNRMSAIAARLPGRTDN 102

Db 61 LRPDVTRKGNFTDDEDTITELHQLVGNRMSAIAARLPGRTDN 102

Search completed: June 24, 2006, 00:05:31

Job time : 51 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: June 23, 2006, 23:55:27 ; Search time 296 Seconds
(without alignments)
803.139 Million cell updates/sec

Title: US-10-521-811-2

Perfect score: 1368

Sequence: 1 MGRAPCCRCMGGLKGGPWTPK.....MDYVLGVFWESGDAQDLPOI 257

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : Uniprot 7.2.*
1: uniprot_sprot.*
2: uniprot_trcemb.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1368	100.0	257	MYB4_ORYSA	07xbh4 oryza sativ
2	933	68.2	277	061x77 WHEAT	061x77 triticum ae
3	835.5	61.1	288	096463 HORVU	096463 hordeum vul
4	827.5	60.5	258	06K186_ORYSA	06K186 oryza sativ
5	709.5	51.9	280	002993_PETRY	002993 petunia hyb
6	697.5	51.0	276	004108_ORYSA	004108 oryza sativ
7	697.5	51.0	276	07XDC7_ORYSA	07XDC7 oryza sativ
8	694	50.7	281	09SLT0_TOBAC	09SLT0 nicotiana t
9	690	50.4	281	09SLT2_TOBAC	09SLT2 nicotiana t
10	687	50.2	265	040174_LYCES	040174 lycopersico
11	684	50.0	277	09SLT1_TOBAC	09SLT1 nicotiana t
12	677.5	49.5	264	09SLT3_SOYBN	09SLT3 glycine max
13	669.5	48.9	278	P93391_TOBAC	P93391 nicotiana t
14	665.5	48.6	264	09XIU9_SOYBN	09XIU9 glycine max
15	661.5	48.4	285	09LTC4_ARYTH	09LTC4 arabidopsis
16	658	48.1	275	09XIU8_SOYBN	09XIU8 glycine max
17	653.5	47.8	253	08LSN7_9ROSI	08LSN7 vitis labru
18	648.5	47.4	270	02LME1_MALDO	02LME1 malus domes
19	646.5	47.3	253	08LSN8_9ROSI	08LSN8 vitis labru
20	646	47.2	233	02VOV6_DAUCA	02VOV6 daucus caro
21	645.5	47.2	232	09XIU5_SOYBN	09XIU5 glycine max
22	640	46.8	273	049744_ARYTH	049744 arabidopsis
23	628.5	45.9	246	09LNC9_ARYTH	09LNC9 arabidopsis
24	623.5	45.6	246	039153_ARYTH	039153 arabidopsis
25	608	44.4	249	09SLX8_ARYTH	09SLX8 arabidopsis
26	595	43.5	157	06OD72_NICBE	06OD72 nicotiana b
27	585.5	42.8	340	06YU06_ORYSA	06YU06 oryza sativ
28	582	42.5	122	039260_ARYTH	039260 arabidopsis
29	576	42.1	345	07XUV5_ORYSA	07XUV5 oryza sativ
30	568	41.5	371	07X793_ORYSA	07X793 oryza sativ
31	563.5	41.2	340	MYB1_MAIZE	P20024 zea mays (m

32	562	41.1	274	2	09SA47_ARYTH	09SA47 arabidopsis
33	561	41.0	272	2	08LEES_ARYTH	08LEES arabidopsis
34	550.5	40.2	357	2	08GUA1_ORYSA	08GUA1 oryza sativ
35	550	40.2	368	2	004141_ORYSA	004141 oryza sativ
36	549	40.1	368	2	06Z414_ORYSA	06Z414 oryza sativ
37	546	39.9	299	2	09M2D9_ARYTH	09M2D9 arabidopsis
38	546	39.9	300	2	06H7S0_ORYTH	06H7S0 oryza sativ
39	544	39.8	267	2	0652E6_ORYSA	0652E6 oryza sativ
40	543	39.7	110	2	084XN1_LOUPR	084XN1 lolium pere
41	541.5	39.6	367	2	084U53_9ASPA	084U53 dendrobium
42	533	39.0	294	2	06R0A6_ARYTH	06R0A6 arabidopsis
43	532	38.9	325	2	06R054_ARYTH	06R054 arabidopsis
44	532	38.9	325	2	09LPE1_ARYTH	09LPE1 arabidopsis
45	532	38.9	336	2	084PP4_LOUYA	084PP4 lotus japon

ALIGNMENTS

RESULT 1
MYB4_ORYSA STANDARD; PRT; 257 AA.
ID MYB4_ORYSA
AC Q7XBH4; O04140; Q7XKW3; Q8A75;
DT 30-AUG-2005, integrated into UniprotKB/Swiss-Prot.
DT 30-AUG-2005, sequence version 2.
DT 07-MAR-2006, entry version 21.
DE Myb-related protein Myb4 (OsmYb4) (Transcription factor RLTR1).
GN Name=MYB4; Synonyms=LTRL; OrderedLocustNames=Os04g43680;
GN ORFNames=OSUNBA0073E02.6;
OX Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade;
OC Eriartoideae; Oryzoae; Oryza.
OX NCBI_TaxId=4530;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA], AND INDUCTION.
RC STRAIN=cv. Japonica / Arborio; TISSUE=coleoptile;
RA Pandolfi D., Solinas G., Valle G., Coraggio I.;
RT "Cloning of a cDNA encoding a novel myb gene highly expressed in cold
RT stressed rice coleoptiles.";
RL (er) Plant Gene Register PCR97-079.
RN [2]
RP NUCLEOTIDE SEQUENCE [MRNA].
RC STRAIN=cv. Japonica;
RA Quanhong Y., Rhee P., Aisheng X.;
RT "MYB-family protein acts as a signal transporter in JA induced
RT resistance.";
RN Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=cv. Japonica / Nipponbare;
RX MEDLINE=22337377; PubMed=12447439; DOI=10.1038/nature01183;
RA Feng Q., Zhang Y., Hao P., Wang S., Fu G., Huang Y., Li Y., Zhu J.,
RA Liu Y., Hu X., Jia P., Zhang Y., Zhao Q., Ying K., Yu S., Tang Y.,
RA Wang Q., Zhang L., Lu Y., Wu J., Lu Y., Zhang L.S., Hu H., Guan D.,
RA Liu X., Zhang L., Li C., Wu Y., Sun T., Lei H., Li T., Hu Z.,
RA Wu M., Zhang R., Zhou B., Chen Z., Chen L., Jin Z., Wang R., Yin H.,
CAI Z., Ren S., Lv G., Gu W., Zhu G., Tu Y., Jia J., Zhang Y.,
RA Chen J., Kang H., Chen X., Shao C., Sun Y., Hu Q., Zhang X., Zhang W.,
RA Wang L., Ding C., Sheng H., Gu J., Chen S., Ni L., Zhu F., Chen Y.,
RA Lan L., Lai Y., Cheng Z., Gu M., Jiang J., Li J., Hong G., Xue Y.,
RA Han B.;
RT "Sequence and analysis of rice chromosome 4.";
RL Nature 420:316-320(2002).
RN [4]
RP NUCLEOTIDE SEQUENCE [MRNA] OF 1-159.
RA Yao Q., Peng R., Xiong A., Li X., Fan H.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [5]
RP FUNCTION, AND INDUCTION.
RX PubMed=14675437; DOI=10.1046/j.1365-313X.2003.01938.x;
RA Yamani C., Locatelli F., Bracale M., Magnani E., Marsoni M.,
RA Onato M., Mattana M., Baldoni E., Coraggio I.;

```

RT "Overexpression of the rice Osmyb4 gene increases chilling and
RT freezing tolerance of Arabidopsis thaliana plants."
RL Plant J. 37:115-127(2004).
CC -1- FUNCTION: Putative transcription factor which is may be involved
CC in cold stress response.
CC -1- SUBCELLULAR LOCATION: Nucleus (Probable).
CC -1- INDUCTION: By cold stress.
CC -1- MISCELLANEOUS: Arabidopsis plants overexpressing MYB4 show dwarf
CC phenotype and increased tolerance to cold and freezing.
CC -1- SIMILARITY: Contains 2 Myb DNA-binding domains.
CC -1- CAUTION: Ref.4 sequence differs from that shown due to a
CC frameshift in position 138.
-----
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CC
CC EMBL: Y11414; CAA72217.1; -; mRNA.
CC EMBL: AY323484; AAP92750.1; -; mRNA.
CC EMBL: AL731616; CAE05446.2; -; Genomic DNA.
CC EMBL: AF467733; AAL78372.1; ALT_FRAME; mRNA.
CC PIR: T03825; T03825.
CC HSSP: P06876; 1GVZ.
CC Gramene: Q7XBH4; -.
CC InterPro: IPR001005; Myb DNA bd.
CC Pfam: PF00249; Myb DNA-binding; 2.
CC SMART, SMO0717; SANT; 2.
CC PROSITE, PS00037; MYB_1; 1.
CC PROSITE, PS00334; MYB_2; 1.
CC PROSITE, PS50090; MYB_3; 2.
CC DNA-binding; Nuclear protein; Transcription; Transcription regulation.
CC CHAIN 1 257 /FTId=PRO_0000197080.
FT DNA_BIND 9 61 Myb 1.
FT DNA_BIND 62 112 Myb 2.
FT CONFLICT 138 159 SAKKPAAPAAAPPASPERGASS -> TRRSQPPPPGRCVA
FT CONFLICT 152 152 S -> L (in Ref. 2).
FT CONFLICT 257 AA; 27914 MW; E2B602B89FC9BC37 CRC64;
SQ SEQUENCE 257 AA; 27914 MW; E2B602B89FC9BC37 CRC64;

Query Match 100.0%; Score 1368; DB 1; Length 257;
Best Local Similarity 100.0%; Pred. No. 2.5e-93;
Matches 257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGRAPCCCKMGLKKGWTPPEEDKVLVAHIQRHGHGNWRALPQOAGILRCGKSCRLRWINY 60
DB 1 MGRAPCCCKMGLKKGWTPPEEDKVLVAHIQRHGHGNWRALPQOAGILRCGKSCRLRWINY 60
QY 61 LRPDIKRGNFSEEDTIIHLHELGNRWSAIAARLPGRDNEIKVWHTHLKKRLDAPA 120
DB 61 LRPDIKRGNFSEEDTIIHLHELGNRWSAIAARLPGRDNEIKVWHTHLKKRLDAPA 120
QY 121 OGCHVAASGGKGGKKPKAKKPAAPASPERGASSVTESSVAASVAEHNAGIS 180
DB 121 OGCHVAASGGKGGKKPKAKKPAAPASPERGASSVTESSVAASVAEHNAGIS 180
QY 121 OGCHVAASGGKGGKKPKAKKPAAPASPERGASSVTESSVAASVAEHNAGIS 180
DB 121 OGCHVAASGGKGGKKPKAKKPAAPASPERGASSVTESSVAASVAEHNAGIS 180
QY 181 SASASVCAKESSFTSASEEFOIDSFWESETTSMPLDGYDVMEPGDAFVAPPSADMDY 240
DB 181 SASASVCAKESSFTSASEEFOIDSFWESETTSMPLDGYDVMEPGDAFVAPPSADMDY 240
QY 241 WLGVMESGEADLPQI 257
DB 241 WLGVMESGEADLPQI 257

RESULT 2
O6IX77 WHEAT PRELIMINARY; PRT; 277 AA.
AC O6IX77
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 18.
DE Transcription factor Myb2.
GN Name=Myb2;

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OS Triticum aestivum (Wheat).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Bep clade;
OC Poideae; Triticeae; Triticum.
OX NCBI_TaxID=4565;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Seed.
RA Chen R., Ni Z., Sun Q.;
RL Submitted (Apr-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Nucleus (By similarity).
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CC
CC EMBL: AY615199; AAT37168.1; -; mRNA.
CC HSSP: Q03237; 1ASJ.
CC Gramene: O6IX77; -.
CC GO: GO:0005634; C:nucleus; IEA.
CC GO: GO:0003677; F:DNA binding; IEA.
CC GO: GO:0045449; P:regulation of transcription; IEA.
CC InterPro: IPR012287; Homeodomain-rel.
CC InterPro: IPR001005; Myb DNA bd.
CC Pfam: PF00249; Myb DNA-binding; 2.
CC SMART, SMO0717; SANT; 2.
CC PROSITE, PS00037; MYB_1; UNKNOWN_1.
CC PROSITE, PS00334; MYB_2; 1.
CC PROSITE, PS50090; MYB_3; 2.
CC DNA-binding; Nuclear protein; Repeat.
CC SEQUENCE 277 AA; 30633 MW; D66F95B71EADAE9 CRC64;
SQ SEQUENCE 277 AA; 30633 MW; D66F95B71EADAE9 CRC64;

Query Match 68.2%; Score 933; DB 2; Length 277;
Best Local Similarity 69.6%; Pred. No. 4.9e-61;
Matches 195; Conservative 16; Mismatches 43; Indels 26; Gaps 9;

QY 1 MGRAPCCCKMGLKKGWTPPEEDKVLVAHIQRHGHGNWRALPQOAGILRCGKSCRLRWINY 60
DB 1 MGRAPCCCKMGLKKGWTPPEEDKVLVAHIQRHGHGNWRALPQOAGILRCGKSCRLRWINY 60
QY 61 LRPDIKRGNFSEEDTIIHLHELGNRWSAIAARLPGRDNEIKVWHTHLKKRLDAPA 120
DB 61 LRPDIKRGNFSEEDTIIHLHELGNRWSAIAARLPGRDNEIKVWHTHLKKRLDAPA 120
QY 121 OGCHVAASGGKGGKKPKAKKPAAPASPERGASSVTESSVAASVAEHNAGIS 167
DB 121 OGCHVAASGGKGGKKPKAKKPAAPASPERGASSVTESSVAASVAEHNAGIS 167
QY 168 SVAEE-HGNAGISSASASVCAKESSFTSA--SEFOIDSFWESETTSMPLDGY-DVSN 223
DB 168 SVAEE-HGNAGISSASASVCAKESSFTSA--SEFOIDSFWESETTSMPLDGY-DVSN 223
QY 181 ASAAEEHGNNG-SASASASVKEE-CFTSSESESEFOIDSEFWSETTSTPLDINDVCM 238
DB 181 ASAAEEHGNNG-SASASASVKEE-CFTSSESESEFOIDSEFWSETTSTPLDINDVCM 238
QY 224 EPGDAFVAPPSADMDYMWLGVMESG-----EADLPQI 257
DB 224 EPGDAFVAPPSADMDYMWLGVMESG-----EADLPQI 257
QY 239 EPHDAF-GKPADGDMVWLKVMFGGGDDNDGALDLPQI 277
DB 239 EPHDAF-GKPADGDMVWLKVMFGGGDDNDGALDLPQI 277

RESULT 3
O96463 HORVU PRELIMINARY; PRT; 288 AA.
AC O96463;
DT 01-FEB-1997, integrated into UniProtKB/TrEMBL.
DT 01-FEB-1997, sequence version 1.
DT 07-FEB-2006, entry version 32.
DE Myb4 transcription factor (Fragment).
GN Name=Myb4;
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Bep clade;
OC Poideae; Triticeae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Endosperm;

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RA Gubler F., Roberte J.K., Jacobsen J.;
 RT "Cloning of a cDNA Encoding a Nobel Myb Expressed in Barley Aleurone
 RL Layer (Accession X99973) (G997-013).";
 CC Plant Physiol. 113:306-306(1997).
 CC
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 CC
 CC EMBL, X99973; CAA6235.1; -; mRNA.
 DR PIR, T05954; T05954.
 DR HSSP, P06876; IMBK.
 DR Gramene, Q96463; -.
 DR GO, GO:0005634; C:nucleus; IEA.
 DR GO, GO:0003677; F:DNA binding; IEA.
 DR GO, GO:0045449; P:regulation of transcription; IEA.
 DR InterPro, IPR012287; Homeodomain-rel.
 DR InterPro, IPR012287; Homeodomain-rel.
 DR Pfam, PF00249; Myb DNA-binding; 2.
 DR SMART, SM00717; SANT; 2.
 DR PROSITE, PS00334; MYB_2; 1.
 DR PROSITE, PS50090; MYB_3; 2.
 DR Nucleic protein.
 FT NON TER 1
 SQ SEQUENCE 288 AA; 31044 MW; 4C0E589A9C5F7D38 CRC64;
 Query Match 61.1%; Score 835.5; DB 2; Length 288;
 Best Local Similarity 64.7%; Pred. No. 8; 7e-54;
 Matches 180; Conservative 12; Mismatches 47; Indels 39; Gaps 7;
 QY 16 PWTPEDEVKLVAHIOHGHGHWRALPKQAGLLRCGKSCRLRWINTYRDIKGNFSEKEE 75
 DB 14 PVDAAECKLVIAHSHGHGHWRALPKQAGLLRCGKSCRLRWINTYRDIKGNFDEEE 73
 QY 76 DTIHLHELGNRMSAIAARLPGRDNEIKVNWHTLKKRLDPAQGGVAAVAGGKHK 135
 DB 74 OSIIOHLOHGNRMSAIAARLPGRDNEIKVNWHTLKKRLDPAQGGVAAVAGGKHK 133
 QY 136 PKSAK-----KPAAPASPERSSASSSVES-SMASSVAEEHGN 176
 DB 134 PAAAPAAAPKRDGKVKMNNLALTPAAPAAAPVSPERSVSTVETSTASAAAEQHN 193
 QY 177 AGISSASASVCAKESSFTSA--SEEFQIDSFWSSTLSPLDGY-DVSMERQDAFVAPP 233
 DB 194 SGSSASASASVKEE-CFTSSSESEEFQIDSFWSSTLSPLDLDVCMERHDAFGKRD 252
 QY 234 SADDMDYLVGFMESEG-----EAQDLPOI 257
 DB 253 G--DMDYVLRFLFMGGGSGSGSDNNHHDGALDLPQI 288
 RESULT 4
 Q6K1S6_ORYSA PRELIMINARY; PRT; 258 AA.
 ID Q6K1S6;
 AC Q6K1S6;
 DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
 DT 05-JUL-2004, sequence version 1.
 DT 07-FEB-2006, entry version 18.
 DE Putative myb protein.
 GN Name=B1215B07.15;
 OS Oryza sativa (Japonica cultivar-group).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BPP clade;
 CC Eubacteriobacteria; Oryzae; Oryza.
 CC NCBI_TaxId=39947;
 RN NUCLEOTIDE SEQUENCE.
 RP Sasaki T., Matsunoto T., Katayose Y.;
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
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DR EMBL, AF006523; BAD23776.1; -; Genomic_DNA.
 DR HSSP, Q03237; 1A5J.
 DR Gramene, Q6K1S6; -.
 DR GO, GO:0005634; C:nucleus; IEA.
 DR GO, GO:0003677; F:DNA binding; IEA.
 DR GO, GO:0045449; P:regulation of transcription; IEA.
 DR InterPro, IPR012287; Homeodomain-rel.
 DR InterPro, IPR012287; Homeodomain-rel.
 DR Pfam, PF00249; Myb DNA-binding; 2.
 DR SMART, SM00717; SANT; 2.
 DR PROSITE, PS00037; MYB_1; UNKNOWN_1.
 DR PROSITE, PS00334; MYB_2; 1.
 DR PROSITE, PS50090; MYB_3; 2.
 DR DNA-binding; Nuclear protein; Repeat.
 SQ SEQUENCE 258 AA; 28469 MW; 61FDB01C586612EB CRC64;
 Query Match 60.5%; Score 827.5; DB 2; Length 258;
 Best Local Similarity 62.1%; Pred. No. 3e-53;
 Matches 169; Conservative 29; Mismatches 45; Indels 29; Gaps 8;
 QY 1 MGRAPCCCKKGLKGGWTEBEDKLVIAHIOHGHGHWRALPKQAGLLRCGKSCRLRWINTY 60
 DB 1 MGRAPCCCKKGLKGGWTEBEDKLVIAHIOHGHGHWRALPKQAGLLRCGKSCRLRWINTY 60
 QY 61 LRPDIKGNFSEKEEDTIIHLHELGNRMSAIAARLPGRDNEIKVNWHTLKKRLDAPA 120
 DB 61 LRPDIKGNFSEKEEDTIIHLHELGNRMSAIAARLPGRDNEIKVNWHTLKKRLDAPA 120
 QY 121 OGQVNAVAGGKHKKPKSAKPPAAAAA-----PPASPERSSASSSVES-SMASSVAEEH 174
 DB 121 SGREAAA-----PKKATKKAQAAVAVADVPTTVSPSEQSLSTTTT--SAATTEEX 171
 QY 175 GNAISSASASVCAKESSFTSA--SEEFQIDSFWSSTLSPLDGYVNE-----PGDAF 229
 DB 172 SYSMASSADHNT---TDSFTS--SEEFQIDSFWSSTLSPLDGYVNE-----PGDAF 226
 QY 230 VAPPSA---DDM-DYVLGFVMESEGAQDLPOI 257
 DB 227 GASPPSSNDMDMDPWLKFLIOAGGMONLPQI 258
 RESULT 5
 Q02993_PETHY PRELIMINARY; PRT; 280 AA.
 ID Q02993_PETHY;
 AC Q02993;
 DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.
 DT 01-NOV-1996, sequence version 1.
 DT 07-FEB-2006, entry version 37.
 DE Protein 2.
 GN Name=myb.Ph2;
 OS Pecunia hybrida (Pecunia).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 CC asterids; lamiales; Solanales; Solanaceae; Pecunia.
 CC NCBI_TaxId=4102;
 RN NUCLEOTIDE SEQUENCE.
 RP STRAIN=V26; TISSUE=Floral;
 RC MEDLINE=94035159; PubMed=8220462;
 RA Avila J., Nieto C., Canas L., Benito M.J., Paz-Ares J.;
 RT "Pecunia hybrida genes related to the maize regulatory C1 gene and to
 animal myb proto-oncogenes.";
 RL Plant J. 3:553-562(1993).
 CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
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 CC EMBL, Z13997; CAA78387.1; -; mRNA.
 DR PIR, S26604; S26604.
 DR HSSP, P06876; IGV2.
 DR TRANSFAC, T02890; -.
 DR GO, GO:0005634; C:nucleus; IEA.

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DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0045449; F:regulation of transcription; IEA.
DR InterPro; IPR012287; Homeodomain-rel.
DR Pfam; PF00249; Myb DNA-binding; 2.
DR SMART; SM00717; SANT; 2.
DR PROSITE; PS00037; MYB_1; UNKNOWN_1.
DR PROSITE; PS00334; MYB_2; 1.
DR PROSITE; PS00390; MYB_3; 2.
DR DNA-binding; Nuclear protein; Repeat.
SQ SEQUENCE 280 AA; 32178 MW; 2A687374F02C25F4 CRC64;

Query Match 51.9%; Score 709.5; DB 2; Length 280;
Best Local Similarity 50.5%; Pred. No. 1.9e-44;
Matches 149; Conservative 36; Mismatches 55; Indels 55; Gaps 10;

QY 1 MGRAPCCCKMGLKKGPMTPPEEDKVLVAHIQRHGHGNWRALPKOAGILRCGSKRLRWNY 60
DB 1 MGRAPCCCKMGLKKGPMTPPEEDKVLVAHIQRHGHGNWRALPKOAGILRCGSKRLRWNY 60
QY 61 LRPDIKRNFSKEEDTIIHLLHGNRWSAIAARLPGRTDNEIKVWHTLKKRLD--A 118
DB 61 LRPDIKRNFSKEEDTIIHLLHGNRWSAIAARLPGRTDNEIKVWHTLKKRLD--A 118
QY 119 PAQGGHVAASGGK--KPKSAK-----KPAASAPASPERSA--SSS 160
DB 121 PPOASKRHSKNNHDSKAPSTSKMLDSSFSFTIOENINPMTC---PNSPORSSESST 176
QY 161 VTSSMASSVAEHNAGISSASVCAKESSFTSASEF-QIDDSFMSSETLSMPLDGY 219
DB 177 VTADSLAAT-----DVTNDQDTFIKHE--MDSYENFPEIDESFMTEDLSMG-DWL 224
QY 220 DVSME-PGDA-----PAPPSADMDYWLGVFMESGEGADLPQ 256
DB 225 DLDMEVAGEKQVQPPYSHDKMGQSDVMGAKLEDMDPMVYVTKAEDLDLPE 279

RESULT 6
ID 004108_ORYSA PRELIMINARY; PRT; 276 AA.
AC 004108;
DT 01-JUL-1997, integrated into UniProtKB/TrEMBL.
DT 01-JUL-1997, sequence version 1.
DT 07-FEB-2006, entry version 37.
DE Myb factor.
GN Name=myb; Synonyms=OSUNBa0055P24.4;
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BBP clade;
OC Ehrharioideae; Oryzaceae; Oryza.
OX NCBI_TaxId=4530;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=coleoptiles;
RX MEDLINE=97375319; PubMed=9235602;
RA Lu Y.-P., Zhen R.-G., Rea P.A.;
RA "Acrt4: a fourth member of the Arabidopsis phosphate transporter gene
RT family.";
RL (ex) Plant Gene Register PCR97-082.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Buell C.R., Yuan Q., Moffat K.S., Hill J.N., Jenkins C.N., Burr P.C.,
RA Helio J., Zismann V., Pail G., Bowman C.L., Fujii C.Y., Vanaken S.E.,
RA Bowman C.L., Craven B., Utecherback T.R., Khalak H., Feldblyum T.V.,
RA Quackebush J., White O., Salzberg S.L., Fraser C.M.;
RL Submitted (Apr-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Buell R.;
RL Submitted (Oct-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
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CC EMBL; Y11550; CAAT72185.1; -; mRNA.
CC EMBL; AC037425; AAG13574.1; -; genomic_DNA.
CC PIR; T03823; T03823.
CC HSSP; P06876; 1GV2.
CC Gramene; 004108; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0045449; F:regulation of transcription; IEA.
DR InterPro; IPR012287; Homeodomain-rel.
DR Pfam; PF00249; Myb DNA-binding; 2.
DR SMART; SM00717; SANT; 2.
DR PROSITE; PS00037; MYB_1; UNKNOWN_1.
DR PROSITE; PS00334; MYB_2; UNKNOWN_1.
DR PROSITE; PS00390; MYB_3; 2.
DR DNA-binding; Nuclear protein; Repeat.
SQ SEQUENCE 276 AA; 30065 MW; 45037ADE5557CF25 CRC64;

Query Match 51.0%; Score 697.5; DB 2; Length 276;
Best Local Similarity 53.2%; Pred. No. 1.4e-43;
Matches 150; Conservative 34; Mismatches 61; Indels 37; Gaps 10;

QY 1 MGRAPCCCKMGLKKGPMTPPEEDKVLVAHIQRHGHGNWRALPKOAGILRCGSKRLRWNY 60
DB 1 MGRAPCCCKMGLKKGPMTPPEEDKVLVAHIQRHGHGNWRALPKOAGILRCGSKRLRWNY 60
QY 61 LRPDIKRNFSKEEDTIIHLLHGNRWSAIAARLPGRTDNEIKVWHTLKKRLD-- 117
DB 61 LRPDIKRNFSKEEDTIIHLLHGNRWSAIAARLPGRTDNEIKVWHTLKKRLD-- 117
QY 118 --APAQGGHVAASGGK--HKPKSAKPA--AAPASPERSA--SSVSSMA 167
DB 121 KLAAGGG--GRRRPHTRKOPAAKSAALVKEATPSVSDTSSGVTGCTVSS--P 174
QY 168 SVAEHNAGISSASVCAKESSFTSASE-----EFOIDSFMSSET--LS 213
DB 175 SSADGDHRRQOQOQTHAAV--KESSFGGELPAAAAAPTAAMDESFWSTEVYGMW 231
QY 214 MPLDGYDVSME-PGDAFVAPPSADMDYWLGVFMESGEGADLPQ 254
DB 232 AGLGDMDELELAIGTSSAAARSDDMEFMLKRLTSGDWRL 273

RESULT 7
ID Q7XDC7_ORYSA PRELIMINARY; PRT; 276 AA.
AC Q7XDC7;
DT 01-OCT-2003, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2003, sequence version 1.
DT 07-FEB-2006, entry version 22.
DE Myb factor.
GN ORFNames=LOC_Os10g33810;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BBP clade;
OC Ehrharioideae; Oryzaceae; Oryza.
OX NCBI_TaxId=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Buell C.R., Wing R.A., McCombie W.R., Messing J., Yuan Q., Ouyang S.;
RL Submitted (May-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NonDerivs License
CC EMBL; AE016959; AAP54284.1; -; genomic_DNA.
CC HSSP; P06876; 1GV2.
DR Gramene; Q7XDC7; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.

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Query Match Similarity 50.4%; Score 690; DB 2; Length 281;
 Best Local Similarity 48.8%; Pred. No. 5, 2e-43;
 Matches 147; Conservative 35; Mismatches 53; Indels 66; Gaps 10

QY 1 MGRAPCCCKMGLKGPWTPPEEDKVLVAHIQRHGHGNRALPRQAGLLRGCKSCLRLWNY 60
 DB 1 MYRAPCCCKMGLKGPWTPPEEDQILVSYIQTHGHGNRALPRKAGLLRGCKSCLRLWNY 60
 QY 61 LRPDIKRNENFSKEEDDTIIHHELLGNRMSAIARLPGLTDEIKNWHMTHLKKRLDAPA 120
 DB 61 LRPDIKRNENFSKEEDDTIIHHELLGNRMSAIARLPGLTDEIKNWHMTHLKKRLK 117
 QY 121 QGSHVAAGGKKPKPK-SAKKPAAL-----AAAPASPERSAS--S 159
 DB 118 --NYGPPQNSKRHSKNLNDKAPSPISQTFNNSDNFSNIEDINGPVTGNSPQRSSSEMS 175
 QY 160 SYTESSMASVAEEHGNMGISASASVCAKESSSF-----TSASEEF--QIDDSFWSFTL 212
 DB 176 TTVTV-----STAMTTITIIDDNMFKQIDEMOSENFPIEIDIESFWTDLL 220
 QY 213 SMPLDGYDVSM--PGDAFVAPAPSA-----DDMDVWLFQFMESGEAQDLP 255
 DB 221 STS--NSTFTFMEGTGGELOVQFPSSVKQESMDMVGAKLEDMDFMVNVFIRSGDLLDP 279
 QY 256 Q 256
 DB 280 E 280

RESULT 10
 Q40174 LYCES
 ID Q40174 LYCES PRELIMINARY; PRT; 265 AA.
 AC Q40174.
 DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.
 DT 01-NOV-1996, sequence version 1.
 DT 07-FEB-2006, entry version 37.
 DE THM18 protein.
 DE Name=THM18;
 GN Name=THM18;
 OS Lycopersicon esculentum (Tomato).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 OC asterids; lamiales; Solanales; Solanaceae; Solanum; Lycopersicon.
 OX NCBI_Taxid=4081;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Hypocotyl; PubMed=8639738;
 RA MEDLINE=96270378; PubMed=8639738;
 RX Lin Q., Hamilton W.D.O., Merryweather A.,
 RT "Cloning and initial characterization of 14 myb-related cDNAs from
 RT tomato (Lycopersicon esculentum, cv Ailsa Craig).";
 RL Plant Mol. Biol. 30:1009-1020(1996).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Hypocotyl;
 RA Lin Q., Hamilton W.D.O., Merryweather A.,
 RT "Sequence analysis of a myb-related cDNA (THM18) from tomato
 RT (Accession No. X98308) (PCR96-060).";
 RL Plant Physiol. 0:0-0(0).
 CC -I- SUBCELLULAR LOCATION: Nuclear (By similarity).
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 CC -----
 DR EMBL, X98308; CAA6952.1; -, mRNA.
 DR PIR, T07395; T07395.
 DR HSSP, P06876; IMBK.
 DR TRANSFAC, T02873; -.
 DR GO, GO:0005634; C:nucleus; IEA.
 DR GO, GO:0003677; F:DNA binding; IEA.
 DR GO, GO:0045449; P:regulation of transcription; IEA.
 DR InterPro, IPR012287; Homeodomain-rel.
 DR InterPro, IPR001005; Myb_DNA_bd.

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DR Pfam: PF00249; Myb DNA-binding; 2.
DR SMART: SM00717; SANT; 2.
DR PROSITE: PS00037; MYB_1; UNKNOWN_1.
DR PROSITE: PS00334; MYB_2; 1.
DR PROSITE: PS00900; MYB_3; 2.
DR DNA-binding; Nuclear protein; Repeat.
SQ SEQUENCE 265 AA; 30406 MW; 2A32CB12DFFED01C CRC64;

Query Match 50.2%; Score 687; DB 2; Length 265;
Best Local Similarity 50.7%; Pred. No. 8e-43;
Matches 143; Conservative 38; Mismatches 57; Indels 44; Gaps 9

QY 1 MGRAPCCERKGLKGPMTPEEDKLVVAHIOHGHGNWRALPQAGILRGCKSCRLLRWY 60
DB 1 MGRAPCCERKGLKGPMTPEEDKLVVAHIOHGHGNWRALPQAGILRGCKSCRLLRWY 60
QY 61 LRPIIKGNFSGKEEDTIIHLLHLLGNWMSIAALPGTDNEIKNVHTHLKKRLADA 120
DB 61 LRPIIKGNFSGKEEDTIIHLLHLLGNWMSIAALPGTDNEIKNVHTHLKKRLADA 117
QY 121 QCGHVAASGKKHKKPK--SAKKPAAAAA-----PPASPERSSASSVTE 163
DB 118 --NYQPQNSKRHSKTSHTSVNKKGPFTSSSNNSDLSSTKQHIKIAFNSPQSSS---E 171
QY 164 SSMASSVAEEHGNAGISSASASVCKKESSFTFSASEEF-QIDDSFMSERTLSMP--LDGY 219
DB 172 MSSVTLVVD-----NQMVIIKEKRIESSSEYFPFKIDESFPADELSTENMTIGH 222
QY 220 D-----VSMPEGDADF-VAPPSADDDMDYVGLGVMESEGAADLPQ 256
DB 223 DQELQVREENVDFITTSKMEEDMDFMVNVFIKTDLPFLPE 264

RESULT 11
Q9SLT1.TOBAC
AC Q9SLT1.TOBAC PRELIMINARY; PRT; 277 AA.
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 01-MAY-2000, sequence version 1.
DT 07-FEB-2006, entry version 29.
DE Myb-related transcription factor LBM2.
GN Name=Lbm2;
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC asterids; lamiales; Solanales; Solanaceae; Nicotiana.
OC NCBI_TaxID=4097;
RN NCUCEOTIDE SEQUENCE.
RP MEDLINE=21066940; PubMed=1148294; DOI=10.1105/epc.12.12.2511;
RX Sugimoco K., Takeda S., Hirochika H.;
RA "Myb-related transcription factor NtMYB2 induced by wounding and
RT elicitors is a regulator of the tobacco retrotransposon Tc1 and
RT defense-related genes."
RL Plant Cell 12:2511-2528(2000).
RC -I SUBCELLULAR LOCATION: Nuclear (By similarity).
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CC
CC EMBL: AB028650; BAAB8222.1; -, mRNA.
DR TRNSP; P06876; IGV2.
DR TRANSFAC; T05249; -.
DR GO: GO:0005634; C:nucleus; IEA.
DR GO: GO:0003677; F:DNA binding; IEA.
DR GO: GO:0045449; P:regulation of transcription; IEA.
DR InterPro; IPR012287; Homeodomain-rel.
DR Pfam; PF00249; Myb DNA-binding; 2.
DR SMART; SM00717; SANT; 2.
DR PROSITE; PS00037; MYB_1; UNKNOWN_1.
DR PROSITE; PS00334; MYB_2; 1.
DR PROSITE; PS00900; MYB_3; 2.

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KM DNA-binding; Nuclear protein; Repeat.
 SQ SEQUENCE 277 AA; 32076 MW; D4F3DFB2B1252885 CRC64;
 Query Match 50.0%; Score 684; DB 2; Length 277;
 Best Local Similarity 48.2%; Pred. No. 1,4e-42;
 Matches 144; Conservative 37; Mismatches 52; Indels 66; Gaps 10;

QY 1 MGRAPCECKMKLKGKGPWTPEDKVLVAHIQRHGNMRLPKOAGLLRCGSKRLRMVY 60
 |||||
 DB 1 MGRAPCECKMKLKGKGPWTPEDKVLVAHIQRHGNMRLPKOAGLLRCGSKRLRMVY 60
 |||||

QY 61 LRDPDKRGNFSKEEDTIIHLHLLGNRMSAIAARLPGRDNEIKVMVTHLKKRLDPA 118
 |||||
 DB 61 LRDPDKRGNFSKEEDTIIHLHLLGNRMSAIAARLPGRDNEIKVMVTHLKKRLDPA 120
 |||||

QY 119 PAQGGVAAASGGKHKRKAAPAAAAA-----PPASPERAS 158
 |||||
 DB 121 PPG-----NPRHSHKNDKSGPTTSSNNSHLFTYQKHIIDSSVPAPNSPQISS 173
 |||||

QY 159 SSVTESSMASVAEHNAGISSASVCAKESSFTSASEF-QIDDSFMSSETLMP-- 215
 |||||
 DB 174 ---TEMSTVTLV-DDH-----QWIKQEE--MESSEYPEIDESFTWTKLSTDN 217
 |||||

QY 216 -LDGYVSMERGA-----FVAPPSADMDYWLGVFMESGEADLPQ 256
 |||||
 DB 218 WSNTHDHVMTADQELQVLPFSSLKENVDMLTTRKEDMDRMVNVFRTDDELPE 276
 |||||

RESULT 12
 Q987E3 SOYBN PRELIMINARY; PRT; 264 AA.
 ID Q987E3 SOYBN
 AC Q987E3
 DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
 DT 01-MAY-2000, sequence version 1.
 DT 07-FEB-2006, entry version 27.
 DE GmMYB29A1 protein.
 GN GmMYB29A1;
 OS Glycine max (soybean).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 OC rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
 OC Glycine.
 OX NCBI_TaxID=3847;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Shimizu T., Fujibe R., Senda M., Ishikawa R., Harada T., Niizeki M.,
 RA Akada S.;
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
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 CC EMBL; AB029160; BAA81731.1; -; Genomic DNA.
 DR EMBL; AB029159; BAA81730.1; -; Genomic DNA.
 DR HSSP; P06876; 1GVD.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR GO; GO:0045449; P:regulation of transcription; IEA.
 DR InterPro; IPR01287; Homeodomain-rel.
 DR Pfam; PR00249; MYB DNA-binding; 2.
 DR SMART; SM00717; SANT; 2.
 DR PROSITE; PS00037; MYB_1; UNKNOWN_1.
 DR PROSITE; PS00334; MYB_2; 1.
 DR PROSITE; PS50090; MYB_3; 2.
 KM DNA-binding; Nuclear protein; Repeat.
 SQ SEQUENCE 264 AA; 30387 MW; A2B710AFECAB66A CRC64;
 Query Match 49.5%; Score 677.5; DB 2; Length 264;
 Best Local Similarity 48.4%; Pred. No. 4.1e-42;
 Matches 138; Conservative 39; Mismatches 57; Indels 51; Gaps 6;

QY 1 MGRAPCECKMKLKGKGPWTPEDKVLVAHIQRHGNMRLPKOAGLLRCGSKRLRMVY 60
 |||||
 DB 1 MGRAPCECKMKLKGKGPWTPEDKVLVAHIQRHGNMRLPKOAGLLRCGSKRLRMVY 60
 |||||

QY 61 LRDPDKRGNFSKEEDTIIHLHLLGNRMSAIAARLPGRDNEIKVMVTHLKKRLDPA 120
 |||||
 DB 61 LRDPDKRGNFSKEEDTIIHLHLLGNRMSAIAARLPGRDNEIKVMVTHLKKRLDPA 116
 |||||

QY 121 QGGVAAASGGKHKRKAAPAAAAAAPPASPERASSVTESSMASVAEHNAGIS 180
 |||||
 DB 117 ---NNSDNRKRVSKPRIRKSDNSSTLTQSEP--TSSGCTTSSDPSSPSE-----G 163
 |||||

QY 181 SASASVCAKESSFTSASEFOIDDSFW-----SETLSMPLDGYVSMERGAAPVAP 232
 |||||
 DB 164 TKMDNMNIRKEDIENETVAKPPIDESFPQETVYDSSSTMOSNSMTISNE-----LAP 218
 |||||

QY 233 PS-----ADMDYWLGVFMESGEADLPQ 256
 |||||
 DB 219 PQYQFNSVETPQQQSVGVNDSKFDGDMDFWYDIFIKSGSIELPE 263
 |||||

RESULT 13
 P93391 TOBAC PRELIMINARY; PRT; 278 AA.
 ID P93391 TOBAC
 AC P93391
 DT 01-MAY-1997, integrated into UniProtKB/TrEMBL.
 DT 01-MAY-1997, sequence version 1.
 DT 07-FEB-2006, entry version 34.
 DE Transcription factor LBM3 (Myb-related transcription factor LBM3).
 GN Name=Myb1; Synonyms=Lbm3;
 OS Nicotiana tabacum (Common tobacco).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 OC asterids; lamids; Solanales; Solanaceae; Nicotiana.
 OX NCBI_TaxID=4997;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Xanthi nc;
 RX MEDLINE=97121500; PubMed=8962166; DOI=10.1073/pnas.93.25.14972;
 RA Yang Y., Kleesig D.F.;
 RT "Isolation and characterization of a tobacco mosaic virus-inducible
 RT myb oncogene homolog from tobacco."
 RL Proc. Natl. Acad. Sci. U.S.A. 93:14972-14977 (1996).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Xanthi nc;
 RA Yang Y., Kleesig D.F.;
 RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RA Sugimoto K., Hirochika H.;
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
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 CC EMBL; U72762; AAB4101.1; -; mRNA.
 DR EMBL; AB028651; BAA88223.1; -; mRNA.
 DR PIR; T03850; T03850.
 DR HSSP; P06876; 1MBK.
 DR TRANSFAC; T02880; -.
 DR TRANSFAC; T02880; -.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR GO; GO:0045449; P:regulation of transcription; IEA.
 DR InterPro; IPR01287; Homeodomain-rel.
 DR InterPro; IPR01005; MYB DNA-binding.
 DR Pfam; PR00249; MYB DNA-binding; 2.
 DR SMART; SM00717; SANT; 2.
 DR PROSITE; PS00037; MYB_1; UNKNOWN_1.
 DR PROSITE; PS00334; MYB_2; 1.
 DR PROSITE; PS50090; MYB_3; 2.
 KM DNA-binding; Nuclear protein; Repeat.

DR GO: GO:0005634; C:nucleus; IEA.
DR GO: GO:0003577; F:DNA binding; IEA.
DR GO: GO:0045449; P:regulation of transcription; IEA.
DR InterPro: IPR012287; Homeodomain-rel.
DR InterPro: IPR001005; Myb DNA bd.
DR Pfam: PF00249; Myb DNA-binding; 2.
DR SMART: SM00717; SANT; 2.
DR PROSITE: PS00037; MYB_1; UNKNOWN_1.
DR PROSITE: PS00334; MYB_2; 1.
DR PROSITE: PS50090; MYB_3; 2.
KW DNA-binding; Nuclear protein; Repeat.
SQ SEQUENCE 285 AA; 32042 MW; 51CEFC6DF50F828 CRC64;

Query Match 48.4%; Score 661.5; DB 2; Length 285;
Best Local Similarity 49.0%; Pred. No. 6,9e-41;
Matches 146; Conservative 25; Mismatches 66; Indels 61; Gaps 6;
QY 1 MGRAPCCCEKMGILKKGPWTPPEEDKVLVAHIQRHGHGNWRALPKOAGLLRCGKSCRLRWINY 60
DB 1 MGRAPCCCEKMGILKKGPWTPPEEDQILVSFILNHGSHNRALPKOAGLLRCGKSCRLRWINY 60
QY 61 LRPDIKRGNEFSKEEDTIIHLHELGNRWSAIAARLPGRTDNEIKVWHTLKKRLDAPA 120
DB 61 LKPDIKRGNFTKEEDAIISLHOILGNRWSAIAAKLPGRTDNEIKVWHTLKKRLDAPY 119
QY 121 QCGHVAASGCKKIKKPKSAKKPAAAAAPASPERSASSSVTSSMASSVAEEHGNAGIS 180
DB 120 QPAKPKTSNKKKGTGTPKS-----ESVITSSNSTRSSESLADS---SNPSES 163
QY 181 SASASYCAKESESFTSASE-----FQIDSFVSET 211
DB 164 LRSTSPSTSEVSSMTLSHDGYSNEINMDNKPQDITITDQCVSFFETFGADIDESFWKET 223
QY 212 LSNPLDGYDVS-----MEPGDAFYAPPAD-----DMDYVLGVFMESGEAODL 254
DB 224 LYSQDEHNYSNDLEVAAGLVEIQEFGNLGSANNEMI FDSEMDFMFDVLARTGGEODL 281

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